

342/615

**FIGURE 339**

GATATTCTTTATTTTAAAGAATCTGAAGTACT**ATG**CATCACTCCCTCCAATGTCCTGGGGCAG  
CCACCAGGCATATTCATCTTTGTGTGTGTTTTCTTTTGCTTTAGCACTGGGGCACTTCTTGC  
TTATTTCTTTGGTAGGAAAGGGGCTCAGTTTGTCTTGTGGGGTTGGTGGCAGGCAGGCCGGCT  
TACGCCTGATACGGCCCTGGGTAGAAAGGGAAGGGAAGATAAACTTTTATACAAATGGGGATA  
GCTGGGGTCTGAGACCTGCTTCCTCAGTAAATTCCTGGGATCTGCCTATACCTTCTTTTCTC  
TAACCTGGCATAACCCTGCTTAAAGCCTCTCAGGGCTTCTCTCTGTTCTTAGGATCAAAGTATT  
TAGAGCTACAAGAGCCCTCATGGTCTGGCCCCCTGCCCCCTGGCCAGCTTCATTGTACATGTG  
GTGTTCTCTTGTCTGTTCTG**TAA**TGTGGTATGCCATGGGGTCTTTGCACAAGCCTTTCCTCTT  
TGGCTGGACACTGTTCCCTGCCCCCCCCATACTCTTCCTACTTAATATGTAGTCATCCTGCAG  
ATTTCAATTCTAACATCATTTTCTCCAGGGATCCTGGCCTGACAGAATCTCATCTTGTTTAAT  
GCTCTCATAAGACCACTTGTTTCCCTTTTGCAGCACTTGCCACTCAGTTGTATCTTTATGTGC  
GTTTGTGGTTGTATGGGTGTGTCTGTTCCCCAGAATGCCAGCTCTGAGCTGCGTGAGGGTC  
AAGGGCATTGCTGTGCCTGCCAGGTATAGTGCCTACATGTGGTGGGTGCTCATGTTTTAGAGA  
CTAAATGGAGGAGGAGATGAGGAAAAGATTGAAATCTCTCAGTTCACCAGATGGTGTAGGGCC  
CAGCATTGTAAATTCACACGTTGACTGTGCTTGTGAATTATCTGGGGATGCAGGTCCTGATTC  
AGTAGGCCCAGGTTGGGCATCTCTAACAACTCCACGTGATGCTGATGCTGGTCCTATGAAC  
TATACTAAATAGTAAGAATCTATGGAGCCAGGCTGGGCATGGTGGCTCACACCTATGATCCCA  
GCACTTTGGGAGGCTGAGGCAGGCTGATCACCTGGAGTCAGGATTTCAAGACTAGCCTGGCCA  
ACATGGTGGAAACCCCATCTGTACTAAAAATACACAAATTAGCTGGGCATGGTGGCACATGCCT  
GTAGTCCCAGCTACTTGGGAGGCTGAAGCAAGAGAATCGCTTGAACCTGGGAGGCGGAGGTTG  
CAGTGAGCCGAGATCAGGCCACTGTATTCCAACCAGGGTGACAGAGTGAGACTCTATGTCCAA  
AAAAAAAAAAAA

343/615

**FIGURE 340**

&gt;&lt;/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71234

&gt;&lt;subunit 1 of 1, 143 aa, 1 stop

&gt;&lt;MW: 15624, pI: 9.58, NX(S/T): 0

MHSLQCPGAATRHIHLCVCF SFALALGHFLLISLVGKGLSLSCGVGGRQAGLRLIRPWVRRE  
GKINFYTN GDSWGLRPASSVKFLGSAYTFFSLTWHTLLKASQGFSLFLGSKYLELQEPSWSGP  
CPPGQLHCTCGVLLSFL**Important features of the protein:****Signal peptide:**

amino acids 1-28

344/615

**FIGURE 341**

CGCCATGGCCGGGCTATCCCGCGGGTCCGCGCGCGCACTGCTCGCCGCCCTGCTGGCGTCGACG  
CTGTTGGCGCTGCTCGTGTGCGCCGCGCGGGGTCGCGGCGGCCGGGACCACGGGGACTGGGAC  
GAGGCCTCCCGGCTGCCGCGCTACCACCCGCGAGGACGCGGCGCGCGTGGCCCGCTTCGTG  
ACGCACGTCTCCGACTGGGGCGCTCTGGCCACCATCTCCACGCTGGAGGCGGTGCGCGGCCGG  
CCCTTCGCCGACGTCCTCTCGCTCAGCGACGGGCCCCCGGGCGCGGGCAGCGGCGTGCCCTAT  
TTCTACCTGAGCCCGCTGCAGCTCTCCGTGAGCAACCTGCAGGAGAATCCATATGCTACACTG  
ACCATGACTTTGGCACAGACCAACTTCTGCAAGAAACATGGATTTGATCCACAAAGTCCCCTT  
TGTGTTACATAATGCTGTCAGGAACCTGTGACCAAGGTGAATGAAACAGAAATGGATATTGCA  
AAGCATTTCGTTATTCATTCGACACCCTGAGATGAAAACCTGGCCTTCCAGCCATAATTGGTTC  
TTTGCTAAGTTGAATATAACCAATATCTGGGTCCTGGACTACTTTGGTGGACCAAAAATCGTG  
ACACCAGAAGAATATTATAATGTCACAGTTCAGTGAAGCAGACTGTGGTGAATTTAGCAACAC  
TTATGAAGTTTCTTAAAGTGGCTCATACACACTTAAAGGCTTAATGTTTCTCTGGAAAGCGT  
CCCAGAATATTAGCCAGTTTTCTGTC

345/615

**FIGURE 342**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71269
><subunit 1 of 1, 220 aa, 1 stop
><MW: 24075, pI: 7.67, NX(S/T): 3
MAGLSRGSARALLAALLASTLLALLVSPARGRGGRDHGDWDEASRLPPLPPREDAARVAR
FVTHVSDWGALATISTLEAVRGRPFADVLSLSDGPPGAGSGVPYFYLSPLQLSVSNLQEN
PYATLTMTLAQTNFCKKHGFDPQSPLCVHIMLSGTVTKVNETEMDIKHSLEFIRHPEMKT
WPSSHNWFFAKLNITNIWVLDYFGGPKIVTPEEYYNVTVQ
```

**Important features of the protein:****Transmembrane domain:**

Amino acids 11-29

**N-glycosylation sites:**

Amino acids 160-164;193-197;216-220

**N-myristoylation sites:**

Amino acids 3-9;7-13;69-75;97-103



346/615

**FIGURE 343**

GGCTGGACTGGAACCTCCTGGTCCCAAGTGATCCACCCGCCTCAGCCTCCCAAGGTGCTGTGAT  
TATAGGTGTAAGCCACCGTGTCTGGCCTCTGAACAACTTTTTTTCAGCAACTAAAAAAGCCACAG  
GAGTTGAACTGCTAGGATTCTGACTATGCTGTGGTGGCTAGTGCTCCTACTCCTACCTACATT  
AAAATCTGTTTTTTGTTCTCTTGTAAGTACCTTTACCTTCCTAACACAGAGGATCTGTCACT  
GTGGCTCTGGCCCAAACCTGACCTTCACTCTGGAACGAGAACAGAGGTTTCTACCCACACCGT  
CCCCTCGAAGCCGGGGACAGCCTCACCTTGCTGGCCTCTCGCTGGAGCAGTGCCCTCACCAAC  
TGTCTCACGTCTGGAGGCACTGACTCGGGCAGTGCAAGGTAGCTGAGCCTCTTGGTAGCTGCGG  
CTTTCAAGGTGGGCCTTGCCCTGGCCGTAGAAGGGATTGACAAGCCCCGAAGATTTTCATAGGCG  
ATGGCTCCCCTGCCCAGGCATCAGCCTTGCTGTAGTCAATCACTGCCCTGGGGCCAGGACGG  
GCCGTGGACACCTGCTCAGAAGCAGTGGGTGAGACATCAGCTGCCCGCCCATCTAACCTTTT  
CATGTCCTGCACATCACCTGATCCATGGGCTAATCTGAACTCTGTCCCAAGGAACCCAGAGCT  
TGAGTGAGCTGTGGCTCAGACCCAGAAGGGGTCTGCTTAGACCACCTGGTTTATGTGACAGGA  
CTTGCAATTCTCCTGGAACATGAGGGAACGCCGGAGGAAAGCAAAGTGGCAGGGAAGGAACTTG  
TGCCAAATTATGGGTGAGAAAAGATGGAGGTGTTGGGTATCACAAGGCATCGAGTCTCCTGC  
ATTCAGTGGACATGTGGGGGAAGGGCTGCCGATGGCGCATGACACACTCGGGACTCACCTCTG  
GGGCCATCAGACAGCCGTTTCCGCCCCGATCCACGTACCAGCTGCTGAAGGGCAACTGCAGGC  
CGATGCTCTCATCAGCCAGGCAGCAGCCAAAATCTGCGATCACCAGCCAGGGGCAGCCGTCTG  
GGAAGGAGCAAGCAAAGTGACCATTTCTCCTCCCTCCTTCCCTCTGAGAGGCCCTCCTATGT  
CCCTACTAAAGCCACCAGCAAGACATAGCTGACAGGGGCTAATGGCTCAGTGTGGCCCAGGA  
GGTCAGCAAGGCCTGAGAGCTGATCAGAAGGGCCTGCTGTGCGAACACGGAAATGCCTCCAGT  
AAGCACAGGCTGCAAAATCCCCAGGCAAAGGACTGTGTGGCTCAATTTAAATCATGTTCTAGT  
AATTGGAGCTGTCCCCAAGACCAAAGGAGCTAGAGCTTGGTTCAAATGATCTCCAAGGGCCCT  
TATACCCAGGAGACTTTGATTTGAATTTGAAACCCCAAATCCAAACCTAAGAACCAGGTGCA  
TTAAGAATCAGTTATTGCCGGGTGTGGTGGCCTGTAATGCCAACATTTTGGGAGGCCGAGGCG  
GGTAGATCACCTGAGGTCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACCCCTGTCTC  
TACTAAAAATACAAAAAACTAGCCAGGCATGGTGGTGTGTGCCTGTATCCCAGCTACTCGGG  
AGGCTGAGACAGGAGAATTACTTGAACCTGGGAGGTGAAGGAGGCTGAGACAGGAGAATCACT  
TCAGCCTGAGCAACACAGCGAGACTCTGTCTCAGAAAAAATAAAAAAAGAATTATGGTTATTT  
GTAA

347/615

**FIGURE 344**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71277
><subunit 1 of 1, 109 aa, 1 stop
><MW: 11822, pI: 8.63, NX(S/T): 0
MLWWLVLLLLPTLKSVFCSLVTSLYLPNTEDLSLWLWPKPDLHSGTRTEVSTHTVPSKPGTAS
PCWPLAGAVPSPTVSRLEALTRAVQVAEPLGSCGFQGGPCPGRRRD
```

**Signal peptide:**  
amino acids 1-15

348/615

**FIGURE 345**

CCGCGCCGCGCAGCCGCTACCGCCGCTGCAGCCGCTTTCCGCGCCCTGGGCGCTCTCGCCGCTCAG  
**CATG**CCACACGCCTTCAAGCCCGGGGACTTGGTGTTCGCTAAGATGAAGGCTTACCCTCACTG  
 GCCTGCCAGGATCGACGACATCGCGGATGGCGCCGTGAAGCCCCACCAACAAGTACCCCAT  
 CTTTTTCTTTGGCACACACGAAACAGCCTTTCCTGGGACCCAAGGACCTGTTCCCTACGACAA  
 ATGTAAAGACAAGTACGGGAAGCCCAACAAGAGGAAAGGCTTCAATGAAGGGCTGTGGGAGAT  
 CCAGAACAACCCCCACGCCAGCTACAGCGCCCTCCGCCAGTGAGCTCCTCCGACAGCGAGGC  
 CCCCAGGGCCAACCCCGCCGACGGCAGTGACGCTGACGAGGACGATGAGGACCGGGGGGTCT  
 GGCCGTACAGCGGTAACCGCCACAGCTGCCAGCGACAGGATGGAGAGCGACTCAGACTCAGA  
 CAAGAGTAGCGACAACAGTGCCCTGAAGAGGAAGACGCGCTGCGCTAAAGATGTCGGTCTCGAA  
 ACGAGCCCCGAAAGGCCTCCAGCGACCTGGATCAGGCCAGCGTGTCCCATCCGAAGAGGAGAA  
 CTCGGAAAGCTCATCTGAGTCGGAGAAGACCAGCGACCAGGACTTCACACCTGAGAAGAAAGC  
 AGCGGTCCGGGCGCCACGGAGGGGCCCTCTGGGGGACGGAAAAAAGAAGGCGCCGTACGC  
 CTCCGACTCCGACTCCAAGGCCGATTTCGGACGGGGCCAAGCCTGAGCCGGTGGCCATGGCGCG  
 GTCGGCGTCTCTCCTCCTCTCTCTCCTCCTCCTCCGACTCCGATGTGTCTGTGAAGAAGCC  
 TCCGAGGGGACAGGAAGCCAGCGGAGAAGCCTCTCCGAAGCCGCGAGGGCGGAAACCGAAGCC  
 TGAACGGCCTCCGTCCAGCTCCAGCAGTGACAGTGACAGCGACGAGGTGGACCGCATCAGTGA  
 GTGGAAGCGGCGGGACGAGGCGCGGAGGCGGAGCTGGAGGCCGGCGGCGGCGAGAGCAGGA  
 GGAGGAGCTGCGGCGCCTGCGGGAGCAGGAGAAGGAGGAGAAGGAGCGGAGGCGCGAGCGGGC  
 CGACCGCGGGGAGGCTGAGCGGGGACGCGGCGGCGAGCGGGGACGAGCTCAGGGAGGACGA  
 TGAGCCCGTCAAGAAGCGGGGACGCAAGGGCCGGGGCCGGGTCCCCCGTCTCCTCTGACTC  
 CGAGCCCGAGGCCGAGCTGGAGAGAGAGGCCAAGAAATCAGCGAAGAAGCCGCAGTCTCAAG  
 CACAGAGCCCCGCCAGGAAACCTGGCCAGAAGGAGAAGAGAGTGCGGCCCCGAGGAGAAGCAACA  
 AGCCAAGCCCGTGAAGGTGGAGCGGACCCGGAAGCGGTCCGAGGGCTTCTCGATGGACAGGAA  
 GGTAGAGAAGAAGAAAGAGCCCTCCGTGGAGGAGAAGCTGCAGAAGCTGCACAGTGAGATCAA  
 GTTTGCCCTAAAGGTCGACAGCCCGGACGTGAAGAGGTGCCTGAATGCCCTAGAGGAGATCGG  
 AACCTGCAGGTGACCTCTCAGATCCTCCAGAAGAACACAGACGTGGTGGCCACCTTGAAGAA  
 GATTGCGCGTTACAAAGCGAACAAGGACGTAATGGAGAAGGCAGCAGAAGTCTATACCCGGCT  
 CAAGTCGCGGGTCTTCGGCCCCAAGATCGAGGCGGTGCAGAAAGTGAACAAGGCTGGGATGGA  
 GAAGGAGAAGGCCGAGGAGAAGCTGGCCGGGAGGAGCTGGCCGGGAGGAGGCCCCCAGGA  
 GAAGGCGGAGGACAAGCCCAGCACCGATCTCTCAGCCCCAGTGAATGGCGAGGCCACATCACA  
 GAAGGGGGAGAGCGCAGAGGACAAGGAGCACGAGGAGGGTCGGGACTCGGAGGAGGGGCCAAG  
 GTGTGGCTCCTCTGAAGACCTGCACGACAGCGTACGGGAGGGTCCCGACCTGGACAGGCCTGG  
 GAGCGACCGGCAGGAGCGCGAGAGGGCACGGGGGACTCGGAGGCCCTGGACGAGGAGAGCT**CG**  
**AG**CCGCGGGCAGCCAGGCCAGCCCCGCCCCGAGCTCAGGCTGCCCTCTCCTTCCCCGGCTC  
 GCAGGAGAGCAGAGCAGAGAACTGTGGGGAACGCTGTGCTGTTTGTATTTGTTCCCTTGGGTT  
 TTTTTTTCCTGCCTAATTTCTGTGATTTCCAACCAACATGAAATGACTATAAACGGTTTTTTA  
 ATGA

349/615

**FIGURE 346**

&gt;&lt;/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71286

&gt;&lt;subunit 1 of 1, 671 aa, 1 stop

&gt;&lt;MW: 74317, pI: 7.61; NX(S/T): 0

MPHAFKPGDLVFAKMKGYPHWPARIDDIADGAVKPPPNKYPIFFFFGTHETAFLGPKDLFPYDK  
CKDKYGKPNKRKGFNEGLWEIQNNPHASYSAPPPVSSSDSEAPEANPADGSDADEDEDDEDRGVM  
AVTAVTATAASDRMESDSDSDKSSDNSGLKRKTPALKMSVSKRARKASSDLQASVSPSEEN  
SESSSESEKTSQDFTPEKKA AVRAPRRGPLGGRKKKKAPSASDSDSKADSDGAKPEPVAMAR  
SASSSSSSSSSSSDSDSVKVKPPRGRKPAEKPLPKPRGRKPKPERPPSSSSSSSDSDSDEVDRISE  
WKRRDEARRRELEARRRREQEEELRRLREQEKEEKERRRERADRGEAERGSGGSSGDELREDD  
EPVKKRGRKGRGRGPPSSSDSEPEAELEREAKKSAKKPQSSSTEPARKPGQKEKVRPEEKQQ  
AKPVKVERTRKRESEGFMSMDRKVEKKKEPSVEEKLQKLHSEIKFALKVDSPDVKRCLNALEELG  
TLQVTSQILQKNTDVVATLKKIRRYKANKDVMKAAEVYTRLKSRVLGPKIEAVQKVNKAGME  
KEKAEKLAGEEELAGEEAPQEKAEKDPSTDLSAPVNGEATSQKGESAEDKEHEEGRDSEEGPR  
CGSSEDLHDSVREGPDLDPRPGSDRQERERARGDSEALDEES

**Signal peptide:**

amino acids 1-13

350/615

**FIGURE 347**

GTTGGTTCTCCTGGATCTTCACCTTACCAACTGCAGATCTTGGGACTCATCAGCCTCAATAATTATATTAAATTA  
ACACCATTTGAAAGAGAACATTGTTTTTCATCATGAATGCTAATAAGATGAAAGACTTAAAGCCAGAAGCCAAGA  
TTTTACCTTTTTCTGCTTTGATGATGCTAAGCATGACCATGTTGTTTCTTCCAGTCACTGGCACTTTGAAGCA  
AAATATTCCAAGACTCAAGCTAACCTACAAAGACTTGCTGCTTCAAATAGCTGTATTCCTTTTTGGGTTTCATC  
AGAAGGACTGGATTTTCAAACCTTCTCTTAGATGAGGAAAGAGGAGGCTGCTCTTGGGAGCCAAAGACCACAT  
CTTTCTACTCAGTCTGGTTGACTTAAACAAAAATTTAAGAAGATTTATTGGCCTGCTGCAAAGGAACGGGTGGA  
ATTATGTAAATTAGCTGGGAAAGATGCCAATACAGAATGTGCAAATTTTCATCAGAGTACTTCAGCCCTATAACAA  
AACTCACATATATGTGTGTGGAACCTGGAGCATTTCATCCAATATGTGGGTATATTGATCTTGGAGTCTACAAGGA  
GGATATTATATTCAAACCTAGACACACATAATTTGGAGTCTGGCAGACTGAAATGTCCTTTCCGATCCTCAGCAGCC  
TTTTGCTTCAGTAATGACAGATGAGTACCTCTACTCTGGAACAGCTTCTGATTTCCCTTGGCAAAGATACTGCATT  
CACTCGATCCCTTGGGCCTACTCATGACCACCCTACATCAGAAGTACATTTTCAGAGCACTACTGGCTCAATTGG  
AGCAAAATTTATTGGAACCTTTCTTCATACCAGACACCTACAATCCAGATGATGATAAAATATATTTCTTCTTTCCG  
TGAATCATCTCAAGAAGGCAGTACCTCCGATAAAACCATCCTTTCTCGAGTTGGAAGAGTTGTGAAGAATGATGT  
AGGAGGACAACGCAGCCTGATAAACAAGTGGACGACTTTTCTTAAAGGCCAGACTGATTTGCTCAATTCCTGGAG  
TGATGGGCAGATACTTACTTTGATGAGCTTCAAGATATTTATTTACTCCCCACAAGAGATGAAAGAAATCCTGT  
AGTATATGGAGTCTTTACTACAACAGCTCCATCTTCAAAGGCTCTGCTGTTTGTGTGTATAGCATGGCTGACAT  
CAGAGCAGTTTTTAATGGTCCATATGCTCATAAGGAAAGTGCAGACCATCGTTGGGTGCAGTATGATGGGAGAAAT  
TCCTTATCCACGGCCTGGTACATGTCCAAGCAAACCTATGACCCACTGATTAAGTCCACCCGAGATTTTCCAGA  
TGATGTCATCAGTTTCATAAAGCGGCACTCTGTGATGTATAAGTCCGTATACCCAGTTGCAGGAGGACCAACGTT  
CAAGAGAATCAATGTGGATTACAGACTGACACAGATAGTGGTGGATCATGTCTATTGCAGAAGATGGCCAGTACGA  
TGTAATGTTTTCTTGGAACAGACATTGGAACCTGCTCAAAGTTGTGAGCATTTCAAAGGAAAAGTGGAAATATGGA  
AGAGGTAGTGCTGGAGGAGTTGCAGATATTCAAGCACTCATCAATCATCTTGAACATGGAATTTGCTCTGAAGCA  
GCAACAATTTGATATTGGTTCCCGAGATGGATTAGTTTCAAGCTCTCCTTGCACAGATGCGACACTTATGGGAAAGC  
TTGCGCAGACTGTTGTCTTGCCAGAGACCCCTACTGTGCCTGGGATGGAAATGCATGCTCTCGATATGCTCCTAC  
TTCTAAAAGGAGAGCTAGACGCCAAGATGTAAATATGGCGACCCAATCACCCAGTCTGGGACATCGAAGACAG  
CATTAGTCATGAACTGCTGATGAAAAGGTGATTTTGGCATTGAATTTAACTCAACCTTTCTGGAATGTATACC  
TAAATCCCAACAAGCAACTATTAAATGGTATATCCAGAGGTGAGGAGTGCAGATCGAGAGGAGTTGAAGCCCGA  
TGAAAGAATCATCAAACCGGAATATGGGCTACTGATTGGAAGTTTGCAGAAGAAGGATTCTGGGATGTATTACTG  
CAAAGCCAGGAGCACACTTTTCATCCACACCATAGTGAAGCTGACTTTGAATGTCATTGAGAATGAACAGATGGA  
AAATACCCAGAGGGCAGAGCATGAGGAGGGGCGAGGTCAAGGATCTATTGGCTGAGTCAAGGTTGAGATACAAGA  
CTACATCCAAATCCTTAGCAGCCCCAACTTCAGCCTCGACAGTACTGCGAACAGATGTGGCACAGGGAGAGCG  
GAGACAGAGAAACAAGGGGGCCCAAGTGGAAAGCACATGAGGAAATGAAGAAGAAACGAAATCGAAGACATCA  
CAGAGACCTGGATGAGCTCCCTAGAGCTGTAGCCACGTTAGTTTCTACTTAATTTAAAGAAAAGAAATTCCTTACC  
TATAAAAACATTGCCTTCTGTTTTGTATATCCCTTATAGTAATTCATAAATGCTTCCCATGGAGTTTGGCTAAGG  
CACAAGACAATAATCTGAATAAGACAATATGTGATGAATATAAGAAAGGGCAAAAAATTCATTTGAACAGTTTT  
CCAAGAACAATCTTGACAAGCAAAGTATAAGAAATATCCTAAAAATAGGGGGTTTACAGTTGTAAATGTTTTA  
TGTTTTGAGTTTTTGGAAATTTATTGTGATGTAATAGTTGAGCTAAGCAAGCCCCGAATTTGATAGTGATAAGGT  
GCTTTATTCCCTCGAATGTCCATTAAGCATGGAATTTACCATGCAAGTTGTGCTATGTTCTTATGAACAGATATAT  
CATTCCTATTGAGAACCAGCTACCTTGTGGTAGGGAATAAGAGGTGAGACACAAATTAAGACAACCTCCCATATC  
AACAGGAACCTTTCTCAGTGAGCCATTCACTCCTGGAGAATGGTATAGGAATTTGGAGAGGTGCATTATTTCTTTC  
TGGCCACTGGGGTTAAATTTAGTGTACTACAACATTGATTTACTGAAGGGCACTAATGTTTCCCCAGGATTTCT  
ATTGACTAGTCAGGAGTAACAGGTTTACAGAGAGAAGTTGGTGTCTAGTTATGTGTTTTTTAGAGTATATACTAA  
GCTCTACAGGGACAGAATGCTTAATAAATACTTTAATAAGATATGGGAAAATATTTAATAAAACAAGGAAAACA  
TAATGATGTATAATGCATCCTGATGGGAAGGCATGCAGATGGGATTTGTTAGAAGACAGAAGGAAAGACAGCCAT  
AAATCTGGCTTTGGGAAAACCTCATATCCCCATGAAAAGGAAGAACAATCACAAATAAAGTGAGAGTAATGTAA  
TGGAGCTCTTTTACTAGGGTATAAGTAGCTGCCAATTTGTAATTCATCTGTTAAAAAAATCTAGATTATAACA  
AACTGCTAGCAAAATCTGAGGAAACATAAATCTTCTGAAGAATCATAGGAAGAGTAGACATTTTATTTATAACC  
AATGATATTTTCAGTATATATTTCTCTCTTTTAAAAAATATTTATCATACTCTGTATATTTTCTTTTACTGC  
CTTTATTTCTCCTGTATATTGGATTTTGTGATTATTTTGTAGTGAATAGGAGAAAACAATATATAACACACAGA  
GAATTAAGAAAATGACATTTCTGGGGAGTGGGGATATATATTTTGTGAATAACAGAACGAGTGTAAATTTAAC  
AACGGAAAGGTTAAATTAACCTCTTTGACATCTTCACTCAACCTTTTCTCATTGCTGAGTTAATCTGTTGTAAT  
GTAGTATTGTTTTTGAATTTAACAATAATAAGCCTGCTACATGT

351/615

**FIGURE 348**

&gt;&lt;/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71883

&gt;&lt;subunit 1 of 1, 777 aa, 1 stop

&gt;&lt;MW: 89651, pI: 7.97, NX(S/T): 3

MNANKDERLKARSQDFHLFPALMMLSMTMLFLPVTGTLKQNIPLKLTYSKDLLLSNSCIPFLG  
SSEGLDFQTLTLLDEERGRLLLGAKDHFLLSLVDLNKNFKKIYWPAAKERVELCKLAGKDANT  
ECANFIRVLQPYNKTHIYVCGTGAFHPICGYIDLGVYKEDIIFKLDTHNLESGRLKCPFDPPQ  
PFASVMTDEYLYSGTASDFLGKDTAFTSLGPTHDDHHYIRTDISEHYWLNKAKFIGTFFIPDT  
YNPDDDKIYFFFRESSQEGSTSDKTILSRVGRVCKNDVGGQRSLINKWTTFLKARLICSIPGS  
DGADTYFDELQDIYLLPTRDERNPVVYGVFTTTSSIFKGSVAVCVYSMADIRAVFNGPYAHKES  
ADHRWVQYDGRIPYPRPGTCPSKTYDPLIKSTRDFPDVISFIKRHSVMYKSVYPVAGGPTFK  
RINVDYRLTQIVVDHVIAEDGQYDVMFLGTDIGTVLKVVSISKEKWNMEEVVLEELQIFKHSS  
IILNMEISLQKQQLYIGSRDGLVQLSLHRCDTYKACADCCLARDPYCAWDGNACSRYPATSK  
RRARRQDVKYGDPITQCWDIEDSISHETADEKVIIFGIEFNSTFLECIPKSQQATIKWYIQRSG  
DEHREELKPDERIIKTEYGLLIRSLQKKDSGMYCKAQEHTFIHTIVKLTLNVIENEQMENTQ  
RAEHEEGQVKDLLAESRLRYKDYIQILSSPNFSLDQYCEQMWHREKRRQRNKGKPKWKHMQEM  
KKKRNRHRHRLDELPRAVAT

**Important features of the protein:****Signal peptide:**

amino acids 1-36

**N-glycosylation sites.**

amino acids 139-142, 607-610, 724-727

**Tyrosine kinase phosphorylation site.**

amino acids 571-576

**Gram-positive cocci surface proteins 'anchoring' hexapeptide.**

amino acids 32-37

352/615

**FIGURE 349**

CCCTGACCTCCCTGAGCCACACTGAGCTGGAAGCCGAGAGGTATCCTGGAGCATGCCACCGCGGGGAGCAGA  
CAACCTCCCAGGTAAGCTGGGAGCAAGACCTGAAGCTGTTTCTTCAGGAGCCTGGTGTATTTTCCCCACCCAC  
CTCAGCAGTTTCAGCCAGCAGGGACTGATCAGGTGTGTCTCTGGAGTGGGAGCAGAAGGCGTGGCTGGCAAGA  
GTGGCCTGGAGAAAGAGGTTTACGCGCTTGACCAGCCGAGCTGCCCGTGACTACAAGATCCAGAACCATGGGCATC  
GGGTGAGGTGGGGGGGCACAGGTGTATGTGCACCTTCTGTCTCAGCAAGAAGAGCTGAGAGAGGGGATCTTGG  
AGCCATTGAGGTTGTATGGAGCTACAGAGGGGAGGAAAGGTATTTTAAGGTAACAGTGTGGCACAATAGTTAA  
GAGCACAGTTTTTGGAGCTAGACCGACATAGGTTCAAATTCTCTTCTGTGCTTCTAGTTCTGTAGCCCCAGGT  
AAGGGAGTGACTTAACCTCTCTGGACTTCAATTCTCTCATCACTAAAGTAGGGCCAATAATAGCACCCACCTCAT  
AGGGAAGATTAAATGACATAATGTATGTATGATGCAACTAGCAAAGTACCAGTCCCATAGTAAGTCATGCCCCACAG  
TATTTCCACCCACCCCTGTTCTCTGCCTTCCCAACCAGGTAAGTGAACGACTGGAGCAGAGGCGGCAGAGGCTT  
CAGAGCGGGAGGCTCCAAGCATAGAACAGAGGTTACAGGAAGTCCGAGAGAGCATCCGCCGGGCACAGGTGAGCC  
AGGTGAAGGGGGCTGCCCGCTGGCCCTGCTGACAGGGGCTGGCTTAGATGTGGAGCGCTGGCTGAAGCCAGCCA  
TGACCCAGGCCCAGGATGAGGTGGAGCAGGAGCGGCGGCTCAGTGAGGCTCGGCTGTCCCAGAGGACCTCTCTC  
CAACCGCTGAGGATGCTGAGCTTCTGACTTTGAGGAATGTGAGGAGACGGGAGAGCTCTTTGAGGAGCCTGCCC  
CCCAAGCCCTGGCCACGAGGGCCCTCCCTGCCCCTGCACACGTGGTATTTTCGTATCAGGCAGGGCGTGAGGATG  
AGCTGACAATCACGGAGGGTGAAGTGGCTGGAGGTCATAGAGGAGGGAGATGCTGACGAATGGGTCAAGGCTCGGA  
ACCAGCACGGCGAGGTAGGCTTTGTCCCTGAGCGATATCTCAACTTCCCGGACCTCTCCCTCCCAGAGAGCAGCC  
AAGACAGTGACAATCCCTGCGGGGACAGAGCCACAGCATTCCTGGCACAGGCCCTGTACAGCTACACCGACAGA  
GTGCAGAGGAGCTGAGCTTCCCTGAGGGGGCACTCATCCGTCTGCTGCCCGGGGCCAAGATGGAGTAGATGACG  
GCTTCTGGAGGGGAGAAATTTGGGGGCGGTGTTGGGGTCTTCCCTCCCTGCTGGTGGAGAGCTGCTTGGCCCCC  
CAGGGCCACCTGAACCTCTCTGACCCTGAACAGATGCTGCCGTCCCTTCTCTCTCCAGCTTCTCCACCTGCAC  
CTACCTCTGTGTTGGATGGGCCCCCTGCACCTGTCTGCTGGGGACAAAGCCCTGGACTTCCCTGGGTTCCTGG  
ACATGATGGCACCTCGACTCAGGCCGATGCGTCCACCACCTCCCCCGCGGCTAAAGCCCCGGATCCTGGCCACA  
CAGATCCCTCACCCTGAAGGCCAGGGAAGCCTTGACCCCACTGATGCTGCTGTCTCTTCAAGCTGTCTCAGA  
CCACACCATCAATGATCCAGAGCAACACAGCCAAAAGCTGGAATCGCCCTTATTTCCACCTCACCTCCAAGGGT  
GGAACTTGCCCTTCCCATTTCTAGAGCTGGAACCCACTCCTTTTTTTCCATTGTTCTATCATCTCTAGGACC  
GGAACCTACTACCTTCTCTTCTGTATGACCTATCTAGGTTGGTGAATGCCTGAAATCTCTGGGGCTGGAAACC  
ATCCATCAAGGTCTCTAGTAGTTCTGCCCCACCTCTTCCCCACCTGGCTCCATGACCCACCCACTCTGGATG  
CCAGGGTCACTGGGGTTGGGCTGGGGAGAGGAACAGGCCCTTGGGAATCAGGAGCTGGAGCCAGGATGCGAAGCAG  
CTGTAATGGTCTGAGCGGATTTATTGACAATGAATAAAGGGCACGAAGGCCAGGCCAGGGCTGGGCTCTTGTG  
CTAAGAGGGGAGGGGGCTACGGTGCTATTGCTTTAGGGGGCCACCAGGGCAGGGGCTGCTCCAGCTGCCAC  
GCTCTATCATATGGAGCGAGGTGTTGGGGAAGGGGGGAGGCAGCCCTGTTGCAGGCAGGGGAAGGAGAAGAGAC  
TGAGGGGCTGTGACCTCTCTGAGGCCCCAGCCTGAGACTGTGCAACTCCAGGTGGAAGTAGAGCTGGTCCCTC  
AGCTGGGGGCACTGCTGTCCAGTGGAGGGGAGGGCTTTACGCCCCACCCACCCCTGGCCCTGCCAGCTGGTAG  
TCCATCAGCACAATGAAGGAGACTTGGAGAAGAGGAAGAATAAAGCTGTTGCTTCTCTCAAGCTGTGTCCAGC  
TTTTCCCTGGGGCTCCAGGACCTTCCCTACCTCCACCACCAACCAAGGGATTTATAGCAAAGGCTAAGCCTGC  
AGTTTACTCTGGGGGTTTCAAGGAGCCGAAAGGCTTAAATAGTTTAAAGTAGGTGATGGGAAGATGAGATTACCTCA  
TTTAGGGCTCAGGCAGACTCACCTCACATACTCCCTGCTCCCTGTGGTAGAGACACCTGAGAGAAAGGGGAGGGG  
TCAACAATGAGAGACCAGGAGTAGGTCTATCAGTCCCCCAGAGTAGAGAGCAATAAGAGCCAGCCAGTGC  
AGTCCCGGCTGTGTTTTCTACCTGGTGATCAGAAGTGTCTGGTTTGCTTGGCTGCCATTTGCCCTTTGAGTGG  
GCAGCCCTGGGCTTGGGCCCCCTCCCTCCGGCCCTCAGTGTGGCTCTGCAGAAGCTCTGGGGTTCCCTTCAAGTG  
CACGAGGGGTTAGGCTGCTGTCCCTGAGTCTCTCATTCTGTACTGGGGGGCTGGCTAGGACCTGGGGCTGTGGCC  
TCTCAGGGGGCAGCCTCTCCATGGCAGGCATCCCTGCCTTGGGCTGCCCTCCCCAGACCCCTGACCACCCCTG  
GGTCTGTCCCCACAGAGCCCCAGCTCCTGTCTGTGGGGGAGCCATCACGGTGTTCGTGCAGTCCATAGCGCT  
TCTCAATGTGTGTACCCGGAACCTGGGAGGGGAGGGAACACTGGGGTTTAGGACCACAACCTCAGAGGCTGCTTG  
GCCCTCCCTCTGACCAGGGACATCTGAGTTTGGTGGCTACTTCCCTCTGGCCTAAGGTAGGGGAGGCCCTTCTC  
AGATTGTGGGGCACATTGTGTAGCCTGACTTCTGCTGGAGCTCCAGTCCAGGAGGAAAGAGCCAAGGCCACTT  
TTGGGATCAGGTGCCTGATCACTGGGCCCCCTACCTCAGCCCCCTTTCCCTGGAGCACCTGCCCCACCTGCCCA  
CAGAGAACACAGTGGTCTCCCTGTCCGGGGGCGGCTTTTTCTTCTTGGAGCGTCCCTGACGGACAAGTGGAG  
GCCTCTTGCTGCGGCTGCAATGGATGCAAGGGGCTGCAGAGCCAGGTGCACTGTGTGATGATGGGAGGGGGCTC  
CGTCTGCAGGCTGGAGGTGGCATCCACACTGGACAGGAGGAGGGAGTGAAGGTAACATTTCCATTTCCCT  
TCATGTTTTGTTTTCTTACGTTCTTTACAGCATGCTCCTTAAACCCAGAGCCCCAATTTCCCAAGCCCCATTT  
TTTCTTGTCTTTATCTAATAAACTCAATATTAAG

353/615

**FIGURE 350**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73401
><subunit 1 of 1, 370 aa, 1 stop
><MW: 40685, pI: 4.53, NX(S/T): 0
MQLAKYQSHSKSCPTVFPPTPVLCLPNQVLQRLEQRRQQASEREAPSIEQRLQEVRESIRRAQ
VSQVKGAAARLALLQGAGLDVERWLKPAMTQAQDEVEQEERLSEARLSQRDLSPTAEDAELSDF
EECEETGELFEFPAPQALATRALPCPAHVVFYQAGREDELTITEGEWLEVIEEGDADEWVKA
RNQHGEVGFVPERYLNFPDLSLPESQSDNPCGAEPTAFLAQALYSYTGQSAEELSFPEGAL
IRLLPRAQDGVDDGFWRGEFGGRVGVFPSLLVEELLGPPGPPPELSDPEQMLPSPSPPSFSPPA
PTSVLDGPPAPVLPGDKALDFPGFLDMMAPRLRPMRPPPPPPAKAPDPGHPDPLT
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354/615

**FIGURE 351A**

CACAGGGAGACCCACAGACACATATGCACGAGAGAGACAGAGGAGAAAGACAGAGACAAAGGCACAGCGGAA  
GAAGGCAGAGACAGGGCAGGCACAGAAGCGGCCACAGAGAGTCCCTACAGAGGGAGAGGCCAGAGAAGCTGCAGA  
AGACACAGGCAGGGAGAGACAAAGATCCAGGAAAGGAGGGCTCAGGAGGAGAGTTTGGAGAAGCCAGACCCCTGG  
GCACCTCTCCCAAGCCCAAGGACTAAGTTTCTCCATTTCTTTAACGGTCTCAGCCCTTCTGAAAACCTTTGCC  
TCTGACCTTGGCAGGAGTCCAAGCCCCAGGCTACAGAGAGGAGCTTCCAAAGCTAGGGTGTGGAGGACTTGGT  
GCCCTAGACGGCCTCAGTCCCTCCCAGCTGCAGTACCAGTGCCATGTCCTCCAGACAGGCTCGCATCCCCGGGAGGGG  
CTTGGCAGGGCGCTGGCTGTGGGGAGCCCAACCTGCTCCCTGCTCCCATTTGTGCCGCTCTCCTGGCTGGTGTG  
GCTGCTTCTGCTACTGCTGGCCTCTCTCCTGCCCTCAGCCCGGCTGGCCAGCCCCCTCCCCGGGAGGAGAGAT  
CGTGTTCAGAGAAAGCTCAACGGCAGCGTCTGCTGGCTCGGGCGCCCCCTGCCAGGCTGTTGTGCCGCTTGCA  
GGCCTTTGGGGAGACGCTGCTACTAGAGCTGGAGCAGGACTCCGGTGTGCAGGTCGAGGGGCTGACAGTGCAGTA  
CCTGGGGCAGGCGCCTGAGCTGCTGGGTGGAGCAGAGCCTGGCACCTACCTGACTGGCACCATCAATGGAGATCC  
GGAGTCGGTGGCATCTCTGCACTGGGATGGGGAGCCCTGTTAGGCGTGTTACAATATCGGGGGGCTGAACTCCA  
CCTCCAGCCCCGGAGGGAGGCCCTAACTCTGCTGGGGGACCTGGGGCTCACATCCTACGCCGAAGAGTCC  
TGCCAGCGGTCAAGGTCCCATGTGCAACGTCAAGGCTCCTCTTGAAGCCCCAGCCCCAGCCCAAGAGCCAA  
GCGCTTTGCTTCACTGAGTAGATTTGTGGAGACACTGGTGGTGGCAGATGACAAGATGGCCGCATTCCACGGTGC  
GGGGCTAAAGCGCTACCTGCTAACAGTGATGGCAGCAGCAGCCAAGGCCCTCAAGCACCCAGCATCCGCAATCC  
TGTCAGCTTGGTGGTGAAGTCCGCTAGTGATCCTGGGGTCAGGCGAGGAGGGGCCCCAAGTGGGGCCAGTGCTGC  
CCAGACCCCTGCGCAGCTTCTGTGCCCTGGCAGCGGGGCCCTCAACACCCCTGAGGACTCGGGCCCTGACCACTTTGA  
CACAGCCATTCTGTTTACCCGTCAGGACCTGTGTGGAGTCTCCACTTGCAGACACGCTGGGTATGGCTGATGTGGG  
CACCGTCTGTGACCCGGCTCGGAGCTGTGCCATTGTGGAGGATGATGGGCTCCAGTCAGCCTTCACTGCTGCTCA  
TGAAGTGGGTGATGCTTCAACATGCTCCATGACAACCTCAAGCCATGCATCAGTTTGAATGGGCCCTTTGAGCAC  
CTCTCGCCATGTCATGGCCCCCTGTGATGGCTCATGTGGATCCTGAGGAGCCCTGGTCCCCCTGAGTGGCCGCTT  
CATCACTGACTTCTGGACAATGGCTATGGGCACTGTCTCTTAGACAAAACAGAGGCTCCATTGCATCTGCCTGT  
GACTTTCCCTGGCAAGGACTATGATGCTGACCGCCAGTGGCAGCTGACCTTCGGGCCCGACTCACGCCATTGTCC  
ACAGCTGCCCGCCGCTGTGCTGCCCTCTGGTGTCTGGCCACCTCAATGGCCATGCCATGTGCCAGACCAACA  
CTCGCCCTGGGCCGATGGCACACCCCTGCGGGCCCGCACAGGCCCTGCATGGGTGGTGCCTGCCATGGACCA  
GCTCCAGGACTTCAATATTCCACAGGCTGGTGGCTGGGGTCCCTGGGGACCATGGGGTACTGCTCTCGGACCTG  
TGGGGTGGTGTCCAGTTCTCCTCCCGAGACTGCACGAGGCCCTGTCCCCCGGAATGGTGGCAAGTACTGTGAGGG  
CCGCCGTACCCGCTTCCGCTCCTGCAACACTGAGGACTGCCAACTGGCTCAGCCCTGACCTTCCGCGAGGAGCA  
GTGTGCTGCCTACAACCACCGCACCGACCTCTTCAAGAGCTTCCAGGGCCCATGGACTGGGTCTCTCGCTACAC  
AGGCGTGGCCCCCAGGACCAAGTGCAAACTCACCTGCCAGGCCCGGGCACTGGGCTACTACTATGTGCTGGAGCC  
ACGGGTGGTAGATGGGACCCCTGTTCCCGGACAGCTCCTCGGTCTGTGTCCAGGGCCGATGCATCCATGCTGG  
CTGTGATCGCATATTGGCTCCAAGAAGAAGTTTGACAAGTGCATGGTGTGCGGAGGGGACGGTTCTGGTTGCAG  
CAAGCAGTCAGGCTCCTTCAGGAAATCAGGTACGGATACAACAATGTGGTCACTATCCCCCGGGGGGCCACCCA  
CATCTTGTTCGGCAGCAGGGAAACCCCTGGCCACCGGAGCTACTTGGCCCTGAAGCTCCAGATGGCTCCTTA  
TGCCCTCAATGGTGAATACACGCTGATGCCCTCCCCACAGATGTGGTACTGCCTGGGGCAGTCAGCTTGCCTTA  
CAGCGGGGCCACTGCAGCCTCAGAGACACTGTCAGGCCATGGGCCACTGGCCAGCCTTTGACACTGCAAGTCTT  
AGTGGCTGGCAACCCCCAGGACACACGCTCCGATACAGCTTCTTCTGCCCCGGCCGACCCCTTCAACGCCACG  
CCCCACTCCCAGGACTGGCTGCACCGAAGAGCACAGATTCTGGAGATCCTTCCGGCGCGCCCTGGGCGGGCAG  
GAAATTAACCTCACTATCCCGGCTGCCCTTTCTGGGCACCGGGGCCCTCGGACTTAGCTGGGAGAAAGAGAGCTT  
CTGTTGCTGCCTCATGCTAAGACTCAGTGGGGAGGGGCTGTGGGCGTGAGACCTGCCCTCCTCTCTGCCCTAAT  
GCGCAGGCTGGCCCTGCCCTGGTTTCTGCCCTGGGAGGCACTGATGGGTAGTGGATGGAAGGGGCTGACAGAC  
AGCCCTCCATCTAAACTGCCCCCTGCTGCCCTGCGGGTACAGGAGGGAGGGGGAAGGCAGGGAGGGGCTGGGCC  
CAGTTGTATTTATTTAGTATTTATTTCACTTTTATTTAGCACAGGGAAGGGGACAAGGACTAGGGTCTGGGGAA  
CCTGACCCCTGACCCCTCATAGCCCTCACCTGGGGCTAGGAAATCCAGGGTGGTGGTGATAGGTATAAGTGGTG  
TGTGTATGCGTGTGTGTGTGTGTGTGAAATGTGTGTGTGCTTATGTATGAGGTACAACCTGTTCTGCTTCTCTC  
TTCCTGAATTTTATTTTGGGAAAAGAAAAGTCAAGGGTAGGGTGGGCCCTCAGGGAGTGAGGGATTATCTTTT  
TTTTTTTTCTTTCTTTCTTTCTTTTGTGAGACAGAATCTCGCTCTGTGCCCCAGGCTGGAGTGAATG  
GCACAATCTCGGCTCACTGCATCTCCGCTCCCGGGTTCAAGTGATTCTCATGCCTCAGCCTCCTGAGTAGCTG  
GGATTACAGGCTCCTGCCACCACGCCCAGCTAATTTTGTGTTTGTGTTTGGAGACAGAGTCTCGCTATTGTC  
ACCAGGGCTGGAATGATTTAGCTCACTGCAACCTTCGCCACCTGGGTCCAGCAATTCTCCTGCCTCAGCCTCC  
CGAGTAGCTGAGATTATAGGCACCTACCACCGCCGCTCAATTTTGTATTTTAGTAGAGACGGGGTTTAC  
CATGTTGGCCAGGCTGGTCTCGAATCCTGACCTTAGGTGATCCACTCGCCTCATCTCCCAAGTGTCTGGGATT  
ACAGGCGTGAGCCACCGTGCCTGGCCAGCCCACTAATTTTGTATTTTGTATAGTAGAGACAGGGTTTACCATGT  
TGCCAGGCTGCTCTTGAATCCTGACCTCAGTAATCGACCTGCCTCGCCCTCCCAAGTGTGGGATTACAGG

**FIGURE 351B**

[illegible]

356/615

**FIGURE 352**

&gt;&gt;/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73492

&gt;&lt;subunit 1 of 1, 837 aa, 1 stop

&gt;&lt;MW: 90167, pI: 8.39, NX(S/T): 1

MSQTGSHPGRGLAGRWLWGAQPCLLLPIVPLSWLVWLLLLLLASLLPSARLASPLPREEEIVF  
 PEKLNGSVLPGSGAPARLLCRLQAFGETLLLELEQDSGVQVEGLTVQYLGQAPELLGGAEPGT  
 YLTGTINGDPESVASLHWDGGALLGVLQYRGAEHLHLQPLEGGTPNSAGGPGAHILRRKSPASG  
 QGPMC NVKAPLGSPSPRRRAKRFASLSRFVETLVVADDKMAAFHGAGLKYLLTVMAAAKA  
 FKHPSIRNPVSLVVTRLVILGSGEEGPQVGPSAAQTLRSFCAWQRLNTPEDSGPDHFDTAIL  
 FTRQDL CGVSTCDTLGMADVGTVCDPARSCAIVEDDGLQSAFTAHELGHVFNMLHDNSKPCI  
 SLNGPLSTSRHVMA PVMAHVDPEEPWSPCSARFITDFLDNGYGHCLLDKPEAPLHLPVTFPGK  
 DYDADRQCQLTFGPDSRHCPQLPPCAALWCSGHLNGHAMCQTKHSPWADGTPCGPAQACMGG  
 RCLHMDQLQDFNIPQAGGWGPWGPWGDCSRTC GGGVQFSSRDCTRPVPRNGGKYCEGRRTFR  
 SCNTEDCPTGSALTFREEQCAAYNHRTDLFKSFPGPMDWVPRYTGVPQDQCKLTCQARALGY  
 YYVLEPRVVDGTPCSPDSSSVCVQGRCIHAGCDRIIGSKKKFDKCMVCGDGS GCSKQSGSFR  
 KFRYGYNNVVTIPAGATHILVRQQGNPGHRSIYLALKLPDGSYALNGEYTLMPSPDVLPGA  
 VSLRYSGATAASETL SGHGPLAQPLTLQVLVAGNPQDTRLRYSFVPRPTPSTPRPTPDWLH  
 RRAQILEILRRRPWAGRK

**Important features of the protein:****Signal peptide:**

amino acids 1-48

**N-glycosylation site.**

amino acids 68-71

**Glycosaminoglycan attachment site**

amino acids 188-191, 772-775

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 182-185

**Tyrosine kinase phosphorylation site.**

amino acids 730-736

**N-myristoylation sites.**

amino acids 5-10, 19-24, 121-126, 125-130, 130-135, 147-152, 167-  
 172, 168-173, 174-179, 323-328, 352-357, 539-544, 555-560, 577-  
 582, 679-684, 682-687, 763-768

**Amidation sites.**

amino acids 560-563, 834-837

**Leucine zipper pattern.**

amino acids 17-38, 24-45

**Neutral zinc metalloproteinases, zinc-binding region signature.**

amino acids 358-367

357/615

**FIGURE 353**

GCGGAACTGGCTCCGGCTGGCACCTGAGGAGCGGCGTGACCCCGAGGGCCCAGGGAGCTGCCC  
GGCTGGCCTAGGCAGGCAGCCGCACCATGGCCAGCACGGCCGTGCAGCTTCTGGGCTTCCTGC  
TCAGCTTCCTGGGCATGGTGGGCACGTTGATCACCACCATCCTGCCGCACTGGCGGAGGACAG  
CGCACGTGGGCACCAACATCCTCACGGCCGTGTCCTACCTGAAAGGGCTCTGGATGGAGTGTG  
TGTGGCACAGCACAGGCATCTACCAGTGCCAGATCTACCGATCCCTGCTGGCGCTGCCCCAAG  
ACCTCCAGGCTGCCCCGCGCCCTCATGGTCATCTCCTGCCTGCTCTCGGGCATAGCCTGCGCCT  
GCGCCGTCAATCGGGATGAAGTGCACGCGCTGCGCCAAGGGCACACCCGCCAAGACCACCTTTG  
CCATCCTCGGCGGCACCCTCTTCATCCTGGCCGGCCTCCTGTGCATGGTGGCCGTCTCCTGGA  
CCACCAACGACGTGGTGCAGAACTTCTACAACCCGCTGCTGCCCAGCGGCATGAAGTTTGAGA  
TTGGCCAGGCCCTGTACCTGGGCTTCATCTCCTCGTCCCTCTCGCTCATTGGTGGCACCTGC  
TTTGCCTGTCTGCCAGGACGAGGCACCCTACAGGCCCTACCAGGCCCCGCCAGGGCCACCA  
CGACCACTGCAAACACCGCACCTGCCTACCAGCCACCAGCTGCCTACAAAGACAATCGGGCCC  
CCTCAGTGACCTCGGCCACGCACAGCGGGTACAGGCTGAACGACTACGTGTGAGTCCCCACAG  
CCTGCTTCTCCCCCTGGGCTGCTGTGGGCTGGGTCCCCGGCGGGACTGTCAATGGAGGCAGGGG  
TTCCAGCACAAAGTTTACTTCTGGGCAATTTTTGTATCCAAGGAAATAATGTGAATGCGAGGA  
AATGTCTTTAGAGCACAGGGACAGAGGGGGAAATAAGAGGAGGAGAAAGCTCTCTATACAAA  
GACTGAAAAAAAAAATCCTGTCTGTTTTTGTATTTATTATATATATTTATGTGGGTGATTTGA  
TAACAAGTTTAAATATAAAGTGAAGTTGGGAGTTTGGTCAGTGGGGTTGGTTTGTGATCCAGGAA  
TAAACCTTGCGGATGTGGCTGTTTATGAAAAAAAAAAAAA

358/615

## **FIGURE 354**

MASTAVQLLGFLLSFLGMVGTLLITTILPHWRRTAHVGTNILTAVSYLKGLWMECVWHSTGIYQ  
CQIYRSLALPQDLQAARALMVISCLLSGIACACAVIGMKCTRCAGTPAKTTFAILGGTLFI  
LAGLLCMVAVSWTTNDVVQNFYNPLLPSGMKFEIGQALYLGFISSLSLIGGTLLCLSCQDEA  
PYRPYQAPPRATTTTANTAPAYQPPAAYKDNRAPSVTSATHSGYRLNDYV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-21

**Transmembrane domains:**

amino acids 82-103, 115-141, 160-182

359/615

**FIGURE 355**

GAGCTCCCCCTCAGGAGCGCGTTAGCTTTCACACCTTCGGCAGCAGGAGGGCGGCAGCTTCTCGC  
AGGCGGCAGGGCGGGCGGCCAGGATC**ATG**TCCACCACCACATGCCAAGTGGTGGCGTTCTCTCC  
TGTCCATCCTGGGGCTGGCCGGCTGCATCGCGGCCACCGGGATGGACATGTGGAGCACCCAGG  
ACCTGTACGACAACCCCGTCACCTCCGTGTTCCAGTACGAAGGGCTCTGGAGGAGCTGCGTGA  
GGCAGAGTTCAGGCTTCACCGAATGCAGGCCCTATTTACCATCCTGGGACTTCCAGCCATGC  
TGCAGGCAGTGCAGGCCCTGATGATCGTAGGCATCGTCCTGGGTGCCATTGGCCTCCTGGTAT  
CCATCTTTGCCCTGAAATGCATCCGCATTGGCAGCATGGAGGACTCTGCCAAAGCCAAACATGA  
CACTGACCTCCGGGATCATGTTCAATTGTCTCAGGTCTTTGTGCAATTGCTGGAGTGTCTGTGT  
TTGCCAACATGCTGGTGACTAACTTCTGGATGTCCACAGCTAACATGTACACCGGCATGGGTG  
GGATGGTGCAGACTGTTCCAGACCAGGTACACATTTGGTGCGGCTCTGTTCTGGGCTGGGTGCG  
CTGGAGGCCTCACACTAATTGGGGGTGTGATGATGTGCATCGCCTGCCGGGGCTGGCACCAG  
AAGAAACCAACTACAAAGCCGTTTCTTATCATGCCTCAGGCCACAGTGTTCCTACAAGCCTG  
GAGGCTTCAAGGCCAGCACTGGCTTTGGGTCCAACACCAAAAACAAGAAGATATACGATGGAG  
GTGCCCCGACAGAGGACGAGGTACAATCTTATCCTTCCAAGCACGACTATGTG**TAA**TGCTCTA  
AGACCTCTCAGCACGGGCGGAAGAACTCCCGGAGAGCTCACCAAAAAACAAGGAGATCCCA  
TCTAGATTTCTTCTTGCTTTTGACTCACAGCTGGAAGTTAGAAAAGCCTCGATTTTCATCTTTG  
GAGAGGCCAAATGGTCTTAGCCTCAGTCTCTGTCTCTAAATATTCCACCATAAAACAGCTGAG  
TTATTTATGAATTAGAGGCTATAGCTCACATTTTCAATCCTCTATTTCTTTTTTTAAATATAA  
CTTTCTACTCTGATGAGAGAATGTGGTTTTAATCTCTCTCTCACATTTTGATGATTAGACAG  
ACTCCCCCTCTTCCTCCTAGTCAATAAACCCATTGATGATCTATTTCCCAGCTTATCCCCAAG  
AAAACCTTTTGAAAGGAAAGAGTAGACCCAAAGATGTTATTTTCTGCTGTTTGAATTTGTCTC  
CCCACCCCCAACTTGGCTAGTAATAAACACTTACTGAAGAAGAAGCAATAAGAGAAAGATATT  
TGTAATCTCTCCAGCCCATGATCTCGGTTTTCTTACACTGTGATCTTAAAAGTTACCAAACCA  
AAGTCATTTTTCAGTTTGAGGCAACCAAACCTTTCTACTGCTGTTGACATCTTCTTATTACAGC  
AACACCATTCTAGGAGTTTCTGAGCTCTCCACTGGAGTCCTCTTTCTGTCGCGGGTCAGAAA  
TTGTCCCTAGATGAATGAGAAAATTATTTTTTTTAAATTTAAGTCCTAAATATAGTTAAATAA  
ATAATGTTTTAGTAAAATGATACACTATCTCTGTGAAATAGCCTCACCCCTACATGTGGATAG  
AAGGAAATGAAAAATAATTGCTTTGACATTGTCTATATGGTACTTTGTAAAGTCATGCTTAA  
GTACAAATTCATGAAAAGCTCACACCTGTAATCCTAGCACTTTGGGAGGCTGAGGAGGAAGG  
ATCACTTGAGCCCAGAAAGTTCGAGACTAGCCTGGGCAACATGGAGAAGCCCTGTCTCTACAAA  
ATACAGAGAGAAAAAATCAGCCAGTCATGGTGGCATAACCTGTAGTCCAGCATTCCGGGAG  
GCTGAGGTGGGAGGATCACTTGAGCCCAGGGAGGTTGGGGCTGCAGTGAGCCATGATCACACC  
ACTGCACTCCAGCCAGGTGACATAGCGAGATCCTGTCTAAAAAATAAAAAATAATAATGGA  
ACACAGCAAGTCCTAGGAAGTAGGTTAAACTAATTCTTTAA

360/615

**FIGURE 356**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73734 .  
><subunit 1 of 1, 261 aa, 1 stop  
><MW: 27856, pI: 8.50, NX(S/T): 1  
MSTTTCQVVAFLLSILGLAGCIAATGMDMWSTQDLYDNPVTSVFQYEGLRSCVRQSSGFTEC  
RPYFTILGLPAMLQAVRALMIVGIVLGAIGLLVSIFALKCIRIGSMEDSAKANMTLTSGIMFI  
VSGLCAIAGVSVFANMLVTNFWMSTANMYTGMGGMVQTVQTRYTFGAALFVGWVAGGLTLIGG  
VMMCIACRGLAPEETNYKAVSYHASGHSVAYKPGGFKASTGFGSNTKNKKIYDGGARTEDEVQ  
SYPSKHDYV

**Signal peptide:**

amino acids 1-23

**Transmembrane domains:**

amino acids 81-100, 121-141, 173-194

361/615

**FIGURE 357**

GGAAAACTGTTCTTCTGTGGCACAGAGAACCCTGCTTCAAAGCAGAAGTAGCAGTTCCGG  
AGTCCAGCTGGCTAAAACTCATCCCAGAGGATAATGGCAACCCATGCCTTAGAAATCGCTGGG  
CTGTTTCTTGGTGGTGGTGGGAATGGTGGGCACAGTGGCTGTCACTGTCATGCCTCAGTGGAGA  
GTGTGGCCTTCATTGAAAACAACATCGTGGTTTTTGAAAACCTTCTGGGAAGGACTGTGGATG  
AATTGCGTGAGGCAGGCTAACATCAGGATGCAGTGCAAAATCTATGATTCCCTGCTGGCTCTT  
TCTCCGGACCTACAGGCAGCCAGAGGACTGATGTGTGCTGCTTCCGTGATGTCTTCTTGGCT  
TTCATGATGGCCATCCTTGGCATGAAATGCACCAGGTGCACGGGGGACAATGAGAAGGTGAAG  
GCTCACATTCTGCTGACGGCTGGAATCATCTTCATCATCACGGGCATGGTGGTGCTCATCCCT  
GTGAGCTGGGTGGCAATGCCATCAGAGATTTCTATAACTCAATAGTGAATGTTGCCCAA  
AAACGTGAGCTTGGAGAAGCTCTCTACTTAGGATGGACCACGGCACTGGTGGTGATTGTTGGA  
GGAGCTCTGTTCTGCTGCGTTTTTGTGCAACGAAAAGAGCAGTAGCTACAGATACTCGATA  
CCTTCCCATCGCACAACCCAAAAAGTTATCACACCGGAAAGAAGTCACCGAGCGTCTACTCC  
AGAAGTCAGTATGTGTAGTTGTGTATGTTTTTTAACTTTACTATAAAGCCATGCAAATGACA  
AAAATCTATATTACTTTCTCAAAATGGACCCCAAAGAACTTTGATTACTGTTCTTAACTGC  
CTAATCTTAATTACAGGAAGTGTGCATCAGCTATTTATGATTCTATAAGCTATTTACAGCAGAA  
TGAGATATTAAACCCAATGCTTTGATTGTTCTAGAAAGTATAGTAATTTGTTTTCTAAGGTGG  
TTCAAGCATCTACTCTTTTTATCATTACTTCAAAATGACATTGCTAAAGACTGCATTATTTT  
ACTACTGTAATTTCTCCACGACATAGCATTATGTACATAGATGAGTGTAACATTTATATCTCA  
CATAGAGACATGCTTATATGGTTTTATTTAAATGAAATGCCAGTCCATTACACTGAATAAAT  
AGAAGTCAACTATTGCTTTTCAGGGAAATCATGGATAGGGTTGAAGAAGGTTACTATTAATTG  
TTTAAAAACAGCTTAGGGATTAATGTCCTCCATTTATAATGAAGATTAAATGAAGGCTTTAA  
TCAGCATTGTAAAGGAAATTGAATGGCTTCTGATATGCTGTTTTTTAGCCTAGGAGTTAGAA  
ATCCTAACTTCTTTATCCTCTTCTCCCAGAGGCTTTTTTTTTCTTGTGTATTAAATTAACATT  
TTTAAACGCAGATATTTTGTCAAGGGGCTTTCGATTCAAACCTGCTTTTCAGGGGCTATACTC  
AGAAGAAAGATAAAAGTGTGATCTAAGAAAAAGTGATGGTTTTTAGGAAAGTGAAAATATTTTT  
GTTTTTGTATTTGAAGAAGAATGATGCATTTTGACAAGAAATCATATATGTATGGATATATTT  
TAATAAGTATTTGAGTACAGACTTTGAGGTTTCATCAATATAAATAAAAGAGCAGAAAAATAT  
GTCTTGGTTTTTCATTTGCTTACCAAAAAACAACAACAAAAAAGTTGTCCTTTGAGAAGTTT  
ACCTGCTCCTATGTGGGTACCTGAGTCAAAATTGTCATTTTTGTTCTGTGAAAAATAAATTTT  
CTTCTTGTACCATTTCTGTTTAGTTTTACTAAAATCTGTAAATACTGTATTTTTCTGTTTATT  
CCAAATTTGATGAACTGACAAATCCAATTTGAAAGTTTGTGTGACGCTGTCTAGCTTAAAT  
GAATGTGTTCTATTTGCTTTATACATTTATATTAATAAATTGTACATTTTTCTAATT



362/615

**FIGURE 358**

&gt;&lt;/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73735

&gt;&lt;subunit 1 of 1, 225 aa, 1 stop

&gt;&lt;MW: 24845, pI: 9.07, NX(S/T): 0

MATHALEIAGLFLGGVGMVGTVAVTVMQWRVSAFIENNIVVFENFWEGGLWMNCVRQANIRMQ  
CKIYDSSLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILLTAGIIF  
IITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIVGGALFCCVFCCN  
EKSSSYRYSIPSHRTTQKSYHTGKKSPSVYSRSQYV

**Signal peptide:**

amino acids 1-17

**Transmembrane domains:**

amino acids 82-101, 118-145, 164-188

363/615

**FIGURE 359**

CCCGCGCCCGGTTCTCCCTCGCAGCACCTCGAAGTGCGCCCTCGCCCTCCTGCTCGCGCCCC  
GCCGCCATGGCTGCCTCCCCGCGCGGCCTGCTGTCCTGGCCCTGACCGGGCTGGCGCTGCTC  
CTGCTCCTGTGCTGGGGCCAGGTGGCATAAGTGGAATAAACTCAAGCTGATGCTTCAAAAA  
CGAGAAGCACCTGTTCCAATAAGACTAAAGTGGCCGTTGATGAGAATAAAGCCAAAGAATTC  
CTTGGCAGCCTGAAGCGCCAGAAGCGGCAGCTGTGGGACCGGACTCGGCCCCGAGGTGCAGCAG  
TGGTACCAGCAGTTTCTCTACATGGGCTTTGATGAAGCGAAATTTGAAGATGACATCACCTAT  
TGGCTTAACAGAGATCGAAATGGACATGAATACTATGGCGATTACTACCAACGTCACCTATGAT  
GAAGACTCTGCAATTGGTCCCCGGAGCCCCCTACGGCTTTAGGCATGGAGCCAGCGTCAACTAC  
GATGACTACTAACCATGACTTGCCACACGCTGTACAAGAAGCAAATAGCGATTCTCTTCATGT  
ATCTCCTAATGCCTTACACTACTTGGTTTCTGATTTGCTCTATTTGAGCAGATCTTTTCTACC  
TACTTTGTGTGATCAAAAAAGAAGAGTTAAACAACACATGTAAATGCCTTTTGATATTTTCAT  
GGGAATGCCTCTCATTTAAAAATAGAAATAAAGCATTTTGTTAAAAAGA

364/615

**FIGURE 360**

&gt;&lt;/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73742 .

&gt;&lt;subunit 1 of 1, 148 aa, 1 stop

&gt;&lt;MW: 17183, pI: 8.77, NX(S/T): 0

MAASPARPAVLALTGLALLLLLCWGPGGISGNKLKLMLQKREAPVPTKTKVAVDENKAKEFLG

SLKRQKRQLWDRTRPEVQQWYQQFLYMGFDEAKFEDDITYWLNDRDRNGHEYYGDYYQRHYDED

SAIGPRSPYGFRRHGASVNYDDY

**Signal peptide:**

amino acids 1-30

365/615

**FIGURE 361**

GAGATTGGAAACAGCCAGGTTGGAGCAGTGAGTGAGTAAGGAAACCTGGCTGCCCTCTCCAGA  
TTCCCCAGGCTCTCAGAGAAGATCAGCAGAAAGTCTGCAAGACCCTAAGAACCATCAGCCCTC  
AGCTGCACCTCCTCCCCTCCAAGGATGACAAAGGCGCTACTCATCTATTTGGTCAGCAGCTTT  
CTTGCCCTAAATCAGGCCAGCCTCATCAGTCGCTGTGACTTGGCCCAGGTGCTGCAGCTGGAG  
GACTTGGATGGGTTTGAGGGTTACTCCCTGAGTGACTGGCTGTGCCTGGCTTTTGTGGAAAGC  
AAGTTCAACATATCAAAGATAAATGAAAATGCGGATGGAAGCTTTGACTATGGCCTCTTCCAG  
ATCAACAGCCACTACTGGTGCAACGATTATAAGAGTTACTCGGAAAACCTTTGCCACGTAGAC  
TGTCAAGATCTGCTGAATCCCAACCTTCTTGCAAGCATCCACTGCGCAAAAAGGATTGTGTCC  
GGAGCACGGGGGATGAACAACCTGGGTAGAATGGAGGTTGCACTGTTCAAGGCCGGCCACTCTCC  
TACTGGCTGACAGGATGCCGCCTGAGATTGAAACAGGGTGCGGGTGCACCGTGGAGTCATTCCA  
AGACTCCTGTCCTCACTCAGGGATTCTTCATTTCTTCTTCCTACTGCCTCCACTTCATGTTAT  
TTTCTTCCCTTCCCATTTACAACATAAACTGACCAGAGCCCCAGGAATAAATGGTTTTCTTGG  
CTTCCTCCTTACTCCCATCTGGACCCAGTCCCCTGGTTCCTGTCTGTTATTTGTAAACTGAGG  
ACCACAATAAAGAAATCTTTATATTTATCG

366/615

**FIGURE 362**

&gt;&lt;/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73746

&gt;&lt;subunit 1 of 1, 148 aa, 1 stop

&gt;&lt;MW: 16896, pI: 6.05, NX(S/T): 1

MTKALLIYLVSSFLALNQASLISRCDLAQVLQLEDLDGFEGYSLSDWLCLAFVESKFNISKIN  
ENADGSFDYGLFQINSHYWCNDYKSYSENLCVDCQDLLNPNNLAGIHCAKRIVSGARGMNNW  
VEWRLHCSGRPLSYWLTGCRLR

**Signal peptide:**

amino acids 1-18

367/615

**FIGURE 363**

TCTGACCTGACTGGAAGCGTCCAAAGAGGGGACGGCTGTCAGCCCTGCTTGACTGAGAACCCAC  
CAGCTCATCCCAGACACCTCATAGCAACCTATTTATACAAAGGGGGAAAGAAACACCTGAGCA  
GAATGGAATCATTATTTTTTTTCCCAAGGAGAAAACCGGGGTAAAGGGAGGGAAGCAATTCAAT  
TTGAAGTCCCTGTGAATGGGCTTTTCTGATTGTAAGTGGGAAGCAGGTCTTGACACGCTGTTG  
GGTGAAACTTGGGTCTGTGGTTTTCTGATTGTAAGTGGGAAGCAGGTCTTGACACGCTGTTG  
GCAAATGTCAGGACCAGGTAAAGTGAAGTGGCAGAAAACTTCCAGGTGGAACAAGCAACCCAT  
GTTCTGCTGCAAGCTTGAAGGAGCCTGGAGCGGGAGAAAAGCTAACTTGAACATGACCTGTTGC  
ATTTGGCAAGTTCTAGCAACATGCTCCTAAGGAAGCGATACAGGCACAGACCATGCAGACTCC  
AGTTCCTCCTGCTGCTCCTGATGCTGGGATGCGTCTCTGATGATGGTGGCGATGTTGCACCCCTC  
CCCACCACACCCCTGCACCAGACTGTCACAGCCCCAAGCCAGCAAGCACAGCCCTGAAGCCAGGT  
ACCGCCTGGACTTTGGGGAATCCCAGGATTGGGTACTGGAAGCTGAGGATGAGGGTGAAGAGT  
ACAGCCCTCTGGAGGGCCTGCCACCCTTTATCTACTGCGGGAGGATCAGTGTCTGGTGGCCG  
TGGCCTTACCCCAGGCCAGAAGGAACCGAGCCAGGGCAGGAGAGGTGGGAGCTACCGCCTCA  
TCAAGCAGCCAAGGAGGCAGGATAAGGAAGCCCCAAAGAGGGGACTGGGGGGCTGATGAGGACG  
GGGAGGTGTCTGAAGAAGAGGAGTTGACCCCGTTACAGCCTGGACCACGTGGCCCTCCAGGAGG  
CACTCAGTGCCCGCATCCCCCTCCAGAGGGCTCTGCCCGAGGTGCGGCACCCACTGTGTCTGC  
AGCAGCACCCCTCAGGACAGCCTGCCCCACAGCCAGCGTCATCCTCTGTTTCCATGATGAGGCCT  
GGTCCACTCTCCTGCGGACTGTACACAGCATCCTCGACACAGTGCCAGGGCCTTCTGAAGG  
AGATCATCCTCGTGGACGACCTCAGCCAGCAAGGACAACCTCAAGTCTGCTCTCAGCGAATATG  
TGGCCAGGCTGGAGGGGGTGAAGTTACTCAGGAGCAACAAGAGGCTGGGTGCCATCAGGGCCC  
GGATGCTGGGGGCCACCAGAGCCACCGGGGATGTGCTCGTCTTCATGGATGCCCACTGCGAGT  
GCCACCAGGCTGGCTGGAGCCCCTCCTCAGCAGAATAGCTGGTGACAGGAGCCGAGTGGTAT  
CTCCGGTGATAGATGTGATTGACTGGAAGACTTTCCAGTATTACCCCTCAAAGGACCTGCAGC  
GTGGGGTGTGGACTGGAAGCTGGATTTCCACTGGGAACCTTTGCCAGAGCATGTGAGGAAGG  
CCCTCCAGTCCCCCATAAGCCCCATCAGGAGCCCTGTGGTGCCCGGAGAGGTGGTGGCCATGG  
ACAGACATTACTTCCAAAACACTGGAGCGTATGACTCTCTTATGTCGCTGCGAGGTGGTGAAA  
ACCTCGAACTGTCTTTCAAGGCCTGGCTCTGTGGTGGCTCTGTTGAAATCCTTCCCTGCTCTC  
GGGTAGGACACATCTACCAAATCAGGATTCCCATTTCCCCCTCGACCAGGAGGCCACCCTGA  
GGAACAGGGTTTCGATTGCTGAGACCTGGCTGGGGTCATTCAAAGAAACCTTCTACAAGCATA  
GCCCAGAGGCCTTCTCCTTGAGCAAGGCTGAGAAGCCAGACTGCATGGAACGCTTGCAGCTGC  
AAAGGAGACTGGGTTGTCGGACATTCCTACTGGTTTCTGGCTAATGTCTACCCTGAGCTGTACC  
CATCTGAACCCAGGCCAGTTTCTCTGGAAAGCTCCACAACACTGGACTTGGGCTCTGTGCAG  
ACTGCCAGGCAGAAGGGGACATCCTGGGCTGTCCCATGGTGTGGCTCCTTGCAGTGACAGCC  
GGCAGCAACAGTACCTGCAGCACACCAGCAGGAAGGAGATTCACTTTGGCAGCCCACAGCACC  
TGTGCTTTGCTGTCAGGCAGGAGCAGGTGATTCTTCAGAACTGCACGGAGGAAGGCCTGGCCA  
TCCACCAGCAGCACTGGGACTTCCAGGAGAATGGGATGATTGTCCACATTCTTTCTGGGAAAT  
GCATGGAAGCTGTGGTGCAAGAAAACAATAAAGATTTGTACCTGCGTCCGTGTGATGGAAAAG  
CCCGCCAGCAGTGCGGATTTGACCAGATAAATGCTGTGGATGAACGATGAATGTCAATGTGAG  
AAGGAAAAGAGAATTTTGGCCATCAAATCCAGCTCCAAGTGAACGTAAAGAGCTTATATATT  
TCATGAAGCTGATCCTTTTGTGTGTGTGCTCCTTGTGTAGGAGAGAAAAAGCTCTATGAAA  
GAATATAGGAAGTTTCTCCTTTTACACCTTATTTTATTGACTGCTGGCTGCTTA

368/615

**FIGURE 364**

&gt;&lt;/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73760 .

&gt;&lt;subunit 1 of 1, 639 aa, 1 stop

&gt;&lt;MW: 73063, pI: 6.84, NX(S/T): 2

MLLRKRYRHRPCRLQFLLLLLMLGCVLMMVAMLHPPHHTLHQTVTAQASKHSPEARYRLDFGE  
SQDWVLEAEDEGEEYSPLLEGLPPFISLREDQLLVAVALPQARRNQSQGRRGGSYRLIKQPRRQ  
DKEAPKRDWGADEEDGEVSEEEELTPFSLDPRGLQEALSARIPLQRALPEVRHPLCLQQHPQDS  
LPTASVILCFHDEAWSTLLRRTVHSILDTVPRAFLKEIILVDDLSQQGQLKSALSEYVARLEGV  
KLLRSNKRLGAIRARMLGATRATGDVLVFMDAHCECHPGWLEPLLSRIAGDRSRVVSVIDVI  
DWKTFQYYPSKDLQRGVLDWKLDHFHWEPLPEHVRKALQSPISPIRSPVVPGEVAMDRHYFQN  
TGAYDSLMSLRGGENLELSFKAWLCGGSVEILPCSRVGHYQYQNDSSHSPLDQEATLRNRVRIA  
ETWLGSFKETFYKHSPEAFSLSKAEKPDCMERLQLQRRLLGCRTFHWFLANVYPELYPSEPRPS  
FSGKLHNTGLGLCADCQAEGDILGCPMVLAPCSDSRQQQYLQHTSRKEIHFGSPQHLCFAVRQ  
EQVILQNCTEEGLAIHQHWDQFQENGMIVHILSGKCMEAVVQENNKDLYLRPCDGKARQQWRF  
DQINAVDER

**Signal peptide:**

amino acids 1-28

369/615

**FIGURE 365**

GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGGCGG  
AGCCAGACGCTGACCACGTTCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTGCCCCGGC  
AGCCGGGAGCCATGCGACCCCAAGGGCCCCCGCCGCTCCCCGCAGCGGCTCCGCGGCCTCCTGC  
TGCTCCTGCTGCTGCAGCTGCCCCGCGCCGTCGAGCGCCTCTGAGATCCCCAAGGGGAAGCAAA  
AGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACAAGGGCCAG  
CAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTCCGGGTACACCTGGGATCC  
CAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGAGGGAAAGCTTTGAGGAGTCCT  
GGACACCCAACTACAAGCAGTGTTTCATGGAGTTCATTGAATTATGGCATAGATCTTGGGAAAA  
TTGCGGAGTGTACATTTACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGTTCAGTGGCT  
CACTTCGGCTAAAATGCAGAAATGCATGCTGTCAGCGTTGGTATTTACATTCAATGGAGCTG  
AATGTTCAGGACCTCTTCCCATTGAAGCTATAATTTATTTGGACCAAGGAAGCCCTGAAATGA  
ATTCAACAATTAATATTCATCGCACTTCTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTG  
GATTAGTGGATGTTGCTATCTGGGTTGGCACTTGTTTCAGATTACCCAAAAGGAGATGCTTCTA  
CTGGATGGAATTCAGTTTCTCGCATCATTATTGAAGAACTACCAAAATTAAATGCTTTAATTTT  
CATTTGCTACCTCTTTTTTTTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAG  
TTTATGTATACATCTGAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCA  
CACTGTTTTTAAATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTT  
TAGTTGGTTAGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTG  
TGGTCTTTTGTTTTTTCTCTTAGTATAGCATTTTTTAAAAAATATAAAAGCTACCAATCTTTG  
TACAATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA



370/615

**FIGURE 366**

&gt;&lt;/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393

&gt;&lt;subunit 1 of 1, 243 aa, 1 stop

&gt;&lt;MW: 26266, pI: 8.43, NX(S/T): 1

MRPQGPAASPQRLRGLLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA  
GVP  
GRDGSPGANVIPGTPGIPGRDGFKEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIAEC  
TFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIYLDQGSPEMNSTI  
NIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEELPK

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 195-217

371/615

**FIGURE 367**

GTTAACCAGCGCAGTCCTCCGTGCGTCCCGCCCGCCGCTGCCCTCACTCCCGGCCAGGATGGC  
ATCCTGTCTGGCCCTGCGCATGGCGCTGCTGCTGGTCTCCGGGGTTCTGGCCCCTGCGGTGCT  
CACAGACGATGTTCCACAGGAGCCCGTGCCACGCTGTGGAACGAGCCGGCCGAGCTGCCGTC  
GGGAGAAGGCCCCGTGGAGAGCACCAGCCCCGGCCGGGAGCCCGTGGACACCGGTCCCCAGC  
CCCCACCGTCGCGCCAGGACCCGAGGACAGCACCGCGCAGGAGCGGCTGGACCAGGGCGGCGG  
GTCGCTGGGGCCCGGCGCTATCGCGGCCATCGTGATCGCCGCCCTGCTGGCCACCTGCGTGGT  
GCTGGCGCTCGTGGTCGTCGCGCTGAGAAAGTTTTCTGCCTCCTGAAGCGAATAAAGGGGCCG  
CGCCCGGCCGCGCGCGACTCGGCAAAAAAAAAAAAAAA

372/615

**FIGURE 368**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76398  
><subunit 1 of 1, 121 aa, 1 stop  
><MW: 12073, pI: 4.11, NX(S/T): 0  
MASCLALRMALLLVSGVLAPAVLTDDVPQEPVPTLWNEPAELPSGEGPVESTSPGREPVDGTP  
PAPTVAPGPEDSTAQERLDQGGGSLGPGAIAAIVIAALLATCVVLALVVVALRKFSAS

**Important features of the protein:****Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 91-110

**Glycosaminoglycan attachment site.**

amino acids 44-47

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 116-119

**N-myristoylation site.**

amino acids 91-96

373/615

**FIGURE 369**

GGCCGTTGGTTGGTGC GCGGCTGAAGGGTGTGGCGCGAGCAGCGTCGTTGGTTGGCCGGCGGC  
GGGCCGGGACGGGGCATGGCCCTGCTGCTGTGCCTGGTGTGCCTGACGGCGGCGCTGGCCACG  
GCTGTCTGCACTGCCACAGCAACTTCTCCAAGAAGTTCTCCTTCTACCGCCACCATGTGAACT  
TCAAGTCCTGGTGGGTGGGCGACATCCCCGTGTCAGGGGCGCTGCTCACCGACTGGAGCGACG  
ACACGATGAAGGAGCTGCACCTGGCCATCCCCGCCAAGATCACCCGGGAGAAGCTGGACCAAG  
TGGCGACAGCAGTGTACCAGATGATGGATCAGCTGTACCAGGGGAAGATGTACTTCCCCGGGT  
ATTTCCCCAACGAGCTGCGAAACATCTTCCGGGAGCAGGTGCACCTCATCCAGAACGCCATCA  
TCGAAAGGCACCTGGCACCAGGCAGCTGGGGAGGAGGGCAGCTCTCCAGGGAGGGACCCAGCC  
TAGCACCTGAAGGATCAATGCCATCACCCCGCGGGGACCTCCCCTAAGTAGCCCCCAGAGGCG  
CTGGGAGTGTTGCCACCGCCCTCCCCTGAAGTTTGCTCCATCTCACGCTGGGGGTCAACCTGG  
GGACCCCTTCCCTCCGGGCCATGGACACACATACATGAAAACCAGGCCGCATCGACTGTCAGC  
ACCGCTGTGGCATCTTCCAGTACGAGACCATCTCCTGCAACAACTGCACAGACTCGCACGTCG  
CCTGCTTTGGCTATAACTGCGAGTAGGGCTCAGGCATCACACCCACCCGTGCCAGGGCCCTAC  
TGTCCTTGGGGTCCAGGCTCTCCTTGGAGGGGCTCCCCGCCTTCCACCTGGCTGTCATCGG  
GTAGGGCGGGGCGCTGGGTTAGGGGCGCACCACTTCCAAGCCTGTGTCCCACAGGTCCTCGG  
CGCAGTGGAAGTCAGCTGTCCAGGGCCTCCTGAACATACATAAATACTGGCACAAGTAAGTCC  
CCTCCTCAAACCAACACAGGCAGTGTGTGTATGTGAGCACCTCGTGGGTAGTATGTGTGGG  
CACAGGCTGGCTCCCTCAGCTCCACGTCCTAGAGGGGCTCCCGAGGAGGTGGAACCTCAACC  
CAGCTCTGCGCAGGAGGCGGCTGCAGTCCTTTTCTCCCTCAAAGGTCTCCGACCCTCAGCTGG  
AGGCGGGCATCTTTCTAAAGGGTCCCCATAGGGTCTGGTTCCACCCCATCCAGGTCTGTGG  
TCAGAGCCTGGGAGGGTTCCCTACGATGGTTAGGGGTGCCCATGGAGGGGCTGACTGCCCA  
CATTGCCTTTTACAGACAGGACACGAGCATGAGGTAAGGCCGCCCTGACCTGGACTTCAGGGGGA  
GGGGGTAAAGGGAGAGAGGAGGGGGGCTAGGGGGTCTCTAGATCAGTGGGGGCACTGCAGGT  
GGGGCTCTCCCTATACCTGGGACACCTGCTGGATGTCACCTCTGCAACCACACCCATGTGGTG  
GTTTCATGAACAGACCACGTCCTCTGCCTTCTCCTGGCCTGGGACACACAGAGCCACCCCGG  
CCTTGTGAGTGACCCAGAGAAGGGAGGCCTCGGGAGAAGGGGTGCTCGTAAGCCAACACCAGC  
GTGCCGCGGCCTGCACACCCCTTCGGACATCCCAGGCACGAGGGTGTCTGGATGTGGCCACAC  
ATAGGACCACACGTCCTCAGCTGGGAGGAGAGGCCTGGGGCCCCCAGGGAGGGAGGCAGGGGGT  
GGGGGACATGGAGAGCTGAGGCAGCCTCGTCTCCCCGCAGCCTGGTATCGCCAGCCTTAAGGT  
GTCTGGAGCCCCCACACTTGGCCAACCTGACCTTGGAAGATGCTGCTGAGTGTCTCAAGCAGC  
ACTGACAGCAGCTGGGCCTGCCCCAGGGCAACGTGGGGGCGGAGACTCAGCTGGACAGCCCT  
GCCTGTCACTCTGGAGCTGGGCTGCTGCTGCCTCAGGACCCCTCTCCGACCCCGGACAGAGC  
TGAGCTGGCCAGGGCCAGGAGGGCGGGAGGGAGGGAATGGGGGTGGGCTGTGCGCAGCATCAG  
CGCCTGGGCAGGTCCGCAGAGCTGCGGGATGTGATTAAAGTCCCTGATGTTTCTC

374/615

**FIGURE 370**

&gt;&lt;/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76399 .

&gt;&lt;subunit 1 of 1, 157 aa, 1 stop

&gt;&lt;MW: 17681, pI: 7.65, NX(S/T): 1

MALLLCLVCLTAALAHGCLHCHSNFSKKFSFYRHHVNFKSWWVGDI PVSGALLTDWSDDTMKE

LHLAIPAKITREKLDQVATAVYQMMDQLYQGKMYFPGYFPNELRNIFREQVHLIQNAIIERHL

APGSWGGGQLSREGPSLAPEGSMPSPRGDLP

**Signal peptide:**

amino acids 1-15

375/615

**FIGURE 371**

GCCGGCTGTGCAGAGACGCC**ATG**TACCGGCTCCTGTCAGCAGTGA CTGCCCCGGGCTGCCGCCC  
CCGGGGGCTTGGCCTCAAGCTGCGGACGACGCGGGGTCCATCAGCGCGCCGGGCTGCCGCCTC  
TCGGCCACGGCTGGGTTCGGGGGCCCTCGGGCTGGGGCTGGGGCTGGCGCTCGGGGTGAAGCTGG  
CAGGTGGGCTGAGGGGCGCGGCCCCGGCGCAGTCCCCCGCGGCCCCCGACCCTGAGGCGTCGC  
CTCTGGCCGAGCCGCCACAGGAGCAGTCCCTCGCCCCGTGGTCTCCGCAGACCCCGGCGCCGC  
CCTGCTCCAGGTGCTTCGCCAGAGCCATCGAGAGCAGCCGCGACCTGCTGCACAGGATCAAGG  
ATGAGGTGGGCGCACCGGGCATAGTGGTTGGAGTTTCTGTAGATGGAAAAGAAGTCTGGTCAG  
AAGGTTTAGGTTATGCTGATGTTGAGAACCGTGTAACCATGTAAACCAGAGACAGTTATGCGAA  
TTGCTAGCATCAGCAAAAGTCTCACCATGGTTGCTCTTGCCAAATTGTGGGAAGCAGGGAAAC  
TGGATCTTGATATTCCAGTACAACATTATGTTCCCGAATTCCCAGAAAAAGAATATGAAGGTG  
AAAAGGTTTCTGTCAACAAGATTACTGATTTCCCATTTAAGTGGAATTCGTCATTATGAAA  
AGGACATAAAAAAGGTGAAAGAAGAGAAAGCTTATAAAGCCTTGAAGATGATGAAAGAGAATG  
TTGCATTTGAGCAAGAAAAAGAAGGCAAAAGTAATGAAAAGAATGATTTTACTAAATTTAAAA  
CAGAGCAGGAGAATGAAGCCAAATGCCGGAATTCAAAACCTGGCAAGAAAAAGAATGATTTTG  
AACAAGGCGAATTATATTTGAGAGAAAAGTTTGAAAATTCAATTGAATCCCTAAGATTATTTA  
AAAATGATCCTTTGTTCTTCAAACCTGGTAGTCAGTTTTTTGTATTCAACTTTTGGCTATACCC  
TACTGGCAGCCATAGTAGAGAGAGCTTCAGGATGTAAATATTTGGACTATATGCAGAAAATAT  
TCCATGACTTGGATATGCTGACGACTGTGCAGGAAGAAAACGAGCCAGTGATTTACAATAGAG  
CAAGG**TAA**ATGAATACCTTCTGCTGTGTCTAGCTATATCGCATCTTAACACTATTTTATTAAT  
TAAAAGTCAAATTTTCTTTGTTTCCATTCCAAAATCAACCTGCCACATTTTGGGAGCTTTTCT  
ACATGTCTGTTTTCTCATCTGTAAAGTGAAGGAAGTAAACATGTTTATAAAGTAAAAAAA

376/615

**FIGURE 372**

&gt;&lt;/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76522 .

&gt;&lt;subunit 1 of 1, 373 aa, 1 stop

&gt;&lt;MW: 41221, pI: 8.54, NX(S/T): 0

MYRLLSAVTARAAAPGGLASSCGRRGVHQRAGLPPLGHGWVGGGLGLGLGLALGVKLAGGLRGA  
APAQSPAAPDPEASPLAEPPEQSLAPWSPQTPAPPSCSRCFARAIESSRDLLHRIKDEVGAPG  
IVVGVSVDGKEVWSEGLGYADVENRVPCKPETVMRIASISKSLTMVALAKLWEAGKLDLDIPV  
QHYVPEFPEKEYEGEKVSVTTRLLISHLSGIRHYEKDIKKVKEEKAYKALKMMKENVAFEQEK  
EGKSNEKNDFTKFKTEQENEAKCRNSKPGKKNDFEQGELYLREKFENSIESLRLFKNDPLFF  
KPGSQFLYSTFGYTLLAAIVERASGCKYLDYMQKIFHDLMLTTVQEENEPVIYNRAR

**Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 39-60

377/615

**FIGURE 373**

GA CTACGGGGAGAGAGAGAGAGACCAGGACAGCTGCTGAGACCTCTAAGAAGTCCAGATACTAA  
GAGCAAAGATGTTTCAAAC TGGGGGCCTCATTGTCTTCTACGGGCTGTTAGCCCAGACCATGG  
CCCAGTTTGGAGGCCTGCCC GTGCCCCTGGACCAGACCCTGCCCTTGAATGTGAATCCAGCCCTG  
CCCTTGAGTCCCACAGGTCTTG CAGGAAGCTTGACAAATGCCCTCAGCAATGGCCTGCTGTCT  
GGGGGCCTGTTGGGCATTCTGGAAAACCTTCCGCTCCTGGACATCCTGAAGCCTGGAGGAGGT  
ACTTCTGGTGGCCTCCTTGGGGGACTGCTTGGAAGTGAAGTACGTCAGTGATTCTTGGCCTGAAC  
AACATCATTGACATAAAGGTC ACTGACCCCCAGCTGCTGGAACCTGGCCTTGTGCAGAGCCCT  
GATGGCCACCGTCTCTATGTCACCATCCCTCTCGGCATAAAGCTCCAAGTGAATACGCCCCCTG  
GTCGGTGCAAGTCTGTTGAGGCTGGCTGTGAAGCTGGACATCACTGCAGAAATCTTAGCTGTG  
AGAGATAAGCAGGAGAGGATCCACCTGGTCCTTGGTGACTGCACCCATTCCCCTGGAAGCCTG  
CAAATTTCTCTGCTTGATGGACTTGGCCCCCTCCCCATTCAAGGTCTTCTGGACAGCCTCACA  
GGGATCTTGAATAAAGTCCTGCCTGAGTTGGTTCAGGGCAACGTGTGCCCTCTGGTCAATGAG  
GTTCTCAGAGGCTTGGACATCACCTGGTGCATGACATTGTTAACATGCTGATCCACGGACTA  
CAGTTTGT CATCAAGGTCTTAAGCCTTCCAGGAAGGGGCTGGCCTCTGCTGAGCTGCTTCCCAG  
TGCTCACAGATGGCTGGCCCATGTGCTGGAAGATGACACAGTTGCCTTCTCTCCGAGGAACCT  
GCCCCCTCTCCTTTCCCACCAGGCGTGTGTAACATCCCATGTGCCTCACCTAATAAAAATGGCT  
CTTCTTATGCA



378/615

**FIGURE 374**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76533
><subunit 1 of 1, 256 aa, 1 stop
><MW: 26713, pI: 5.62, NX(S/T): 0
MFQTGGLIVFYGLLAQTMAQFGGLPVPLDQTLPLNVNPPALPLSPTGLAGSLTNALSNGLL
SGLLGILENLPLLDILKPGGGTSGLLGGLLGKVTSTVIPGLNNIIDIKVTDLPQLLELGL
VQSPDGHRLYVTIPLGIKLQVNTPLVGASLLRLAVKLDITAEILAVRDKQERIHVLGDC
THSPGSLQISLLDGLGPLPIQGLLDLSLTGILNKVLPPELVQGNVCPLVNEVLRGLDITLVH
DIVNMLIHGLQFVIKV
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-19

**Transmembrane domain:**

Amino acids 79-97

**N-myristoylation sites:**

Amino acids 46-52;49-55;58-64;62-68;66-72;80-86;81-87;  
82-88;85-91;86-92;89-95;202-208;233-239

379/615

**FIGURE 375**

AGTTCTGAGAAAGAAGGAAATAAACACAGGCACCAAACCACTATCCTAAGTTGACTGTCCTTT  
AAATATGTCAAGATCCAGACTTTTTCAGTGTCACCTCAGCGATCTCAACGATAGGGATCTTGTG  
TTTGCCGCTATTCCAGTTGGTGCTCTCGGACCTACCATGCGAAGAAGATGAAATGTGTGTAAA  
TTATAATGACCAACACCCTAATGGCTGGTATATCTGGATCCTCCTGCTGCTGGTTTTGGTGGC  
AGCTCTTCTCTGTGGAGCTGTGGTCCTCTGCCTCCAGTGCTGGCTGAGGAGACCCCGAATTGA  
TTCTCACAGGCGCACCATGGCAGTTTTTGGCTGTTGGAGACTTGGACTCTATTTATGGGACAGA  
AGCAGCTGTGAGTCCAACCTGTTGGAATTCACCTTCAAACCTCAAACCCCTGACCTATATCCTGT  
TCCTGCTCCATGTTTTGGCCCTTTAGGCTCCCCACCTCCATATGAAGAAATTGTAAAAACAAC  
CTGATTTTAGGTGTGGATTATCAATTTAAAGTATTAACGACATCTGTAATTCCAAAACATCAA  
ATTTAGGAATAGTTATTTTCAGTTGTTGGAAATGTCCAGAGATCTATTCATATAGTCTGAGGAA  
GGACAATTCGACAAAAGAATGGATGTTGGAAAAAATTTTGGTCATGGAGATGTTTAAATAGTA  
AAGTAGCAGGCTTTTGATGTGTCACTGCTGTATCATACTTTTATGCTACACAACCAAATTAAT  
GCTTCTCCACTAGTATCCAAACAGGCAACAATTAGGTGCTGGAAGTAGTTTCCATCACATTTA  
GGACTCCACTGCAGTATACAGCACACCATTTTCTGCTTTAAACTCTTTCCTAGCATGGGGTCC  
ATAAAAATTATTATAATTTAACAATAGCCCAAGCCGAGAATCCAACATGTCCAGAACCAGAAC  
CAGAAAGATAGTATTTGAATGAAGGTGAGGGGAGAGAGTAGGAAAAAGAAAAGTTTGGAGTTG  
AAGGGTAAAGGATAAATGAAGAGGAAAAGGAAAAGATTACAAGTCTCAGCAAAAACAAGAGGT  
TTTATGCCCAACCTGAAGAGGAAGAAATTGTAGATAGAAGGTGAAGGAGATTGCTGAAGATA  
TAGAGCACATATAATGCCAACACGGGGAGAAAAGAAAATTTCCCCTTTTACAGTAATGAATGT  
GGCCTCCATAGTCCATAGTGTTTCTCTGGAGCCTCAGGGCTTGGCATTATTTGCAGCATCATG  
CTAAGAACCTTCGGCATAGGTATCTGTTCCCATGAGGACTGCAGAAGTAGCAATGAGACATCT  
TCAAGTGGCATTTTGGCAGTGGCCATCAGCAGGGGGACAGACAAAACATCCATCACAGATGA  
CATATGATCTTCAGCTGACAAATTTGTTGAACAAAACAATAAACATCAATAGATATCTAAAAA

380/615

**FIGURE 376**

&gt;&lt;/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77303 .

&gt;&lt;subunit 1 of 1, 146 aa, 1 stop

&gt;&lt;MW: 16116, pI: 4.99, NX(S/T): 0

MSRSRLFSVTSIAISTIGILCLPLFQLVLSDLPCCEEDEMCVNYNDQHPNGWYIWILLLLVLVAA  
LLCGAVVLCLQCWLRRPRIDSHRRTMAVFAVGDLDSIYGTEAAVSPTVGIHLQTQTPDLYPVP  
APCFGPLGSPPPYEEIVKTT

**Signal peptide:**

amino acids 1-29

**Transmembrane domain:**

amino acids 52-70

381/615

**FIGURE 377**

CGCGGATCGGACCCCAAGCAGGTCTGGCGGCGGCGGCAGGAGAGCGGGCCGGGCGTCAGCTCCTCG  
ACCCCCGTGTCGGGCTAGTCCAGCGAGGCGGACGGGCGGCGTGGGCCC**ATG**GCCAGGCCCGGC  
ATGGAGCGGTGGCGCGACCGGCTGGCGCTGGTGACGGGGGCGCTCGGGGGGCATCGGCGCGGCC  
GTGGCCCGGGCCCTGGTCCAGCAGGGACTGAAGGTGGTGGGCTGCGCCCGCACTGTGGGCAAC  
ATCGAGGAGCTGGCTGCTGAATGTAAGAGTGCAGGCTACCCCGGGACTTTGATCCCCTACAGA  
TGTGACCTATCAAATGAAGAGGACATCCTCTCCATGTTCTCAGCTATCCGTTCTCAGCACAGC  
GGTGTAGACATCTGCATCAACAATGCTGGCTTGGCCCGGCGCTGACACCCTGCTCTCAGGCAGC  
ACCAGTGGTTGGAAGGACATGTTCAATGTGAACGTGCTGGCCCTCAGCATCTGCACACGGGAA  
GCCTACCAGTCCATGAAGGAGCGGAATGTGGACGATGGGCACATCATTAACATCAATAGCATG  
TCTGGCCACCGAGTGTTACCCCTGTCTGTGACCCACTTCTATAGTGCCACCAAGTATGCCGTC  
ACTGCGCTGACAGAGGGACTGAGGCAAGAGCTTCGGGAGGCCAGACCCACATCCGAGCCACG  
TGCATCTCTCCAGGTGTGGTGGAGACACAATTCGCCTTCAAACCTCCACGACAAGGACCCTGAG  
AAGGCAGCTGCCACCTATGAGCAAATGAAGTGTCTCAAACCCGAGGATGTGGCCGAGGCTGTT  
ATCTACGTCCTCAGCACCCCCGCACACATCCAGATTGGAGACATCCAGATGAGGCCACGGAG  
CAGGTGACCT**TAG**TGACTGTGGGAGCTCCTCCTTCCCTCCCCACCCTTCATGGCTTGCCTCCTG  
CCTCTGGATTTTAGGTGTTGATTTCTGGATCACGGGATAACCACTTCTGTCCACACCCCGACC  
AGGGGCTAGAAAATTTGTTTGAGATTTTATATCATCTTGTCAAATTGCTTCAGTTGTAAATG  
TGAAAAATGGGCTGGGGAAAGGAGGTGGTGTCCCTAATTGTTTTACTTGTTAACTTGTTCTTG  
TGCCCCCTGGGCACTTGGCCTTTGTCTGCTCTCAGTGTCTTCCCTTTGACATGGGAAAGGAGTT  
GTGGCCAAAATCCCCATCTTCTTGACCTCAACGTCTGTGGCTCAGGGCTGGGGTGGCAGAGG  
GAGGCCTTACCTTATATCTGTGTTGTTATCCAGGGCTCCAGACTTCCTCCTCTGCCTGCCCC  
ACTGCACCCTCTCCCCCTTATCTATCTCCTTCTCGGCTCCCCAGCCCAGTCTTGGCTTCTTGT  
CCCCTCCTGGGGTCATCCCTCCACTCTGACTCTGACTATGGCAGCAGAACACCAGGGCCTGGC  
CCAGTGGATTTTCATGGTGATCATTAAGAAAGAAATCGCAACCAAAAAAAAAA

382/615

**FIGURE 378**

MARPGMERWRDRLALVTGASGGIGA A VARALVQQGLKVVG CARTVGNIEELAAECKSAGYPGT  
LIPYRC DLSNEEDILSMFSAIRSQHSGVDICINNAGLARPD TLLSGSTSGWKDMFNVNVLALS  
ICTREAYQSMKERNVDDGHIININSMGHRVLP LSVTHFY SATKYAVTALTEGLRQELREAQT  
HIRATCISPGVVETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVLSTPAHIQIGDIQ  
MRPTEQVT

**Important features of the protein:**

**Signal peptide:**

amino acids 1-17

**N-myristoylation sites.**

amino acids 18-24, 21-27, 22-28, 24-30, 40-46, 90-96, 109-115,  
199-205

**Short-chain alcohol dehydrogenase.**

amino acids 30-42, 104-114

383/615

**FIGURE 379**

GAGCGGAGTAAAATCTCCACAAGCTGGGAACAAACCTCGTCCCAACTCCCACCCACCGGCGTT  
TCTCCAGCTCGATCTGGAGGCTGCTTCGCCAGTGTGGGACGCAGCTGACGCCCGCTTATTAGC  
TCTCGCTGCGTCGCCCCGGCTCAGAAGCTCCGTGGCGGGCGGACCGTGACGAGAAGCCCACG  
GCCAGCTCAGTTCTCTTCTACTTTGGGAGAGAGAGAAAGTCAGATGCCCTTTTAACTCCCT  
CTTCAAACTCATCTCCTGGGTGACTGAGTTAATAGAGTGGATACAACCTTGCTGAAGATGAA  
GAATATACAATATTGAGGATATTTTTTCTTTTTTTTTTCAAGTCTTGATTTGTGGCTTACCT  
CAAGTTACCATTTTTTCAAGTCAAGTCTGTTTGTGTTGCTTCTTCAGAAATGTTTTTACAATCTC  
AAGAAAAAATATGTCCAGAAATTGAGTTTACTGTTGCTTGATTTGGACTCATTTGGGGATT  
GATGTTACTGCACTATACTTTTCAACAACCAAGACATCAAAGCAGTGTCAAGTTACGTGAGCA  
AATACTAGACTTAAGCAAAAGATATGTTAAAGCTCTAGCAGAGGAAAATAAGAACACAGTGGA  
TGTCGAGAACGGTGCTTCTATGGCAGGATATGCGGATCTGAAAAGAACAATTGCTGTCTTCT  
GGATGACATTTTGCAACGATTGGTGAAGCTGGAGAACAAAGTTGACTATATTGTTGTGAATGG  
CTCAGCAGCCAACACCACCAATGGTACTAGTGGGAATTTGGTGCCAGTAACCACAAATAAAAG  
AACGAATGTCTCGGGCAGTATCAGATAGCAGTTGAAAATCACCTTGCTGCTGCCATCCACTG  
TGGATTATATCCTATGGCAGAAAAGCTTTATAATTGCTGGCTTAGGACAGAGCAATACTTTAC  
AATAAAAGCTCTACACATTTTCAAGGAGTATGCTGGATTCATGGAACCTCTAATTCTGTACATA  
AAAATTTTAAAGTTATTTGTTTGCTTTCAAGGCAAGTCTGTTCAATGCTGTACTATGTCCTTAA  
AGAGAATTTGGTAACTTGGTTGATGTGGTAAGCAGATAGGTGAGTTTTGTATAAATCTTTTGT  
GTTTGAGATCAAGCTGAAATGAAAACACTGAAAACATGGATTCATTTCTATAACACATTTAT  
TTAAGTATATAACACGTTTTTTGGACAAGTGAAGAATGTTTAATCATTCTGTCAATTTGTTCTC  
AATAGATGTAACCTGTTAGACTACGGCTATTTGAAAAAATGTGCTTATTGTACTATATTTTGT  
ATTCCAATTATGAGCAGAGAAAGGAAATATAATGTTGAAAATAATGTTTTGAAATCATGACCC  
AAAGAATGTATTGATTTGCACTATCCTTCAGAATAACTGAAGGTTAATTATTGTATATTTTAA  
AAAATTACACTTATAAGAGTATAATCTTGAAATGGGTAGCAGCCACTGTCCATTACCTATCGT  
AAACATTGGGGCAATTTAATAACAGCATTAAAATAGTTGTAACTCTAATCTTATACTTATTG  
AAGAATAAAAGATATTTTTATGATGAGAGTAACAATAAAGTATTCATGATTTTTTACATACAT  
GAATGTTCAATTTAAAAGTTTAATCCTTTGAGTGTCTATGCTATCAGGAAAGCACATTATTTCC  
ATATTTGGGTAAATTTTGCTTTTATTATATTGGTCTAGGAGGAAGGGACTTTGGAGAATGGAA  
CTCTTGAGGACTTTAGCCAGGTGTATATAATAAAGGTACTTTTGTGCTGCATTAAATTGCTTG  
GAAAGTGTTAACATTATATTATATAAGAGTATCCTTTATGAAATTTTGAATTTGTATAACAGA  
TGCATTAGATATTCATTTTATATAATGGCCACTTAAAAAAGAACATTTAAAATATAAACTAT  
GAAGATTGACTATCTTTTCAGGAAAAAAGCTGTATATAGCACAGGGAACCCTAATCTTGGGTA  
ATTCTAGTATAAAACAAATTATACTTTTATTTAAATTTCCCTTGTAGCAAATCTAATTGCCAC  
ATGGTGCCCTATATTTCATAGTATTTATTCTCTATAGTAAGTGCCTTAAGTGCAGCTAGCTTCT  
AGATTTAGACTATATAGAATTTAGATATTGTATTGTTTCGTCATTATAATATGCTACCACATGT  
AGCAATAATTACAATATTTTATTTAAATAAATATGTGAAATATTGTTTCATGAAAGACAGATT  
TCCAAATCTCTCTTCTCTCTGTACTGTCTACCTTTATGTGAAGAAATTAATTATATGCCA  
TTGCCAGGT

384/615

**FIGURE 380**

&gt;&lt;/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77648

&gt;&lt;subunit 1 of 1, 140 aa, 1 stop

&gt;&lt;MW: 15668, pI: 10.14, NX(S/T): 5

MFFTISRKNMSQKLSLLLLVFGLIWGLMLLHYTFQQPRHQSSVKLREQILDLSKRYVKALAE

NKNTVDVENGASMAGYADLKRTIAVLLDDILQRLVKLENKVDYIVVNGSAANTTNGTSGNLVP

VTTNKRTNVSGSIR

**Important features of the protein:****Signal peptide:**

amino acids 1-26

385/615

**FIGURE 381**

AACTTCTAC**ATG**GGCCTCCTGCTGCTGGTGCTCTTCCTCAGCCTCCTGCCGGTGGCCTACACC  
ATCATGTCCCTCCCACCCTCCTTTGACTGCGGGCCGTTTCAGGTGCAGAGTCTCAGTTGCCCGG  
GAGCACCTCCCCTCCCGAGGCAGTCTGCTCAGAGGGCCTCGGCCCAAGAATTCAGTTCTGGTT  
TCATGCCAGCCTGTAAAAGGCCATGGAACCTTTGGGTGAATCACCGATGCCATTTAAGAGGGTT  
TTCTGCCAGGATGGAAATGTTAGGTCGTTCTGTGTCTGCGCTGTTCAATTCAGTAGCCACCAG  
CCACCTGTGGCCGTTGAGTGCTTGAAAT**GA**AGGAAGTGAAGAAATTAATTTCTCATGTATTTTT  
CTCATTTATTTATTAATTTTTTAAGTATAGTTGTACATATTTGGGGGTACATGTGATATTTGG  
ATACATGTATACAATATATAATGATCAAATCAGGGTAAGTGGGATATCCATCACATCAAACAT  
TTATTTTTTATTCTTTTTAGACAGAGTCTCACTCTGTCAACCAGGCTGGAGTGCAGTGGTGCC  
ATCTCAGCTTACTGCAACCTCTGCCTGCCAGGTTCAAGCGATTCTCATGCCTCCACCTCCCAA  
GTAGCTGGGACTACAGGCATGCACCACAATGCCCAACTAATTTTTGTATTTTTAGTAGAGACG  
GGGTTTTGCCATGTTGCCCAGGCTGGCCTTGAACTCCTGGCCTCAAACAATCCACTTGCCTCG  
GCCTCCCAAAGTGTTATGATTACAGGCGTGAGCCACCGTGCCTGGCCTAAACATTTATCTTTT  
CTTTGTGTTGGGAACCTTGAAATTATACAATGAATTATTGTTAACTGTCATCTCCCTGCTGTG  
CTATGGAACACTGGGACTTCTTCCCTCTATCTAACTGTATATTTGTACCAGTTAACCAACCGT  
ACTTCATCCCCACTCCTCTCTATCCTTCCCAACCTCTGATCACCTCATTCTACTCTCTACCTC  
CATGAGATCCACTTTTTTAGCTCCCATGTGAGTAAGAAAATGCAATATTTGTCTTTCTGTG  
CCTGGCTTATTTCACTTAACATAATGACTTCCTGTTCCATCCATGTTGCTGCAAATGACAGGA  
TTTCGTTCTTAATTTCAATTAAATAACCACACATGGCAAAAA



386/615

**FIGURE 382**

MGLLLLVLFLSLLPVAYTIMSLPPSFDCGPFRVSVAREHLPSRGSLLRGPRPRIPLVSCQ  
PVKGHGTLGESPMFPKRVFCQDGNVRSFCVCAVHFSSHQPPVAVECLK

**Important features of the protein:**

**Signal peptide:**

amino acids 1-18

**N-myristoylation site.**

amino acids 86-92

**Zinc carboxypeptidases, zinc-binding region 2 signature.**

amino acids 68-79

387/615

**FIGURE 383**

TTCTGAAGTAACGGAAGCTACCTTGTATAAAGACCTCAACACTGCTGACCATGATCAGCGCAG  
CCTGGAGCATCTTCCTCATCGGGACTAAAATTGGGCTGTTCCCTTCAAGTAGCACCTCTATCAG  
TTATGGCTAAATCCTGTCCATCTGTGTGTCGCTGCGATGCGGGTTTCATTTACTGTAATGATC  
GCTTTCTGACATCCATTCCAACAGGAATACCAGAGGATGCTACAACCTCTACCTTCAGAACA  
ACCAAATAAATAATGCTGGGATTCCCTCAGATTTGAAAACTTGCTGAAAGTAGAAAAGAATAT  
ACCTATACCACAACAGTTTAGATGAATTTCCCTACCAACCTCCCAAAGTATGTAAAAGAGTTAC  
ATTTGCAAGAAAATAACATAAGGACTATCACTTATGATTCACTTTCAAAAATCCCTATCTGG  
AAGAATTACATTTAGATGACAACCTGTCTCTGCAGTTAGCATAGAAGAGGGAGCATTCGGAG  
ACAGCAACTATCTCCGACTGCTTTTCCTGTCCCGTAATCACCTTAGCACAAATCCCTGGGGTT  
TGCCCAGGACTATAGAAGAACTACGCTTGGATGATAATCGCATATCCACTATTTTCATCACCAT  
CTCTTCAAGGTCTCACTAGTCTAAAACGCCTGGTTCTAGATGGAAACCTGTTGAACAATCATG  
GTTTAGGTGACAAAGTTTTCTTCAACCTAGTTAATTTGACAGAGCTGTCCCTGGTGCGGAATT  
CCCTGACTGCTGCACCAGTAAACCTTCCAGGCACAAACCTGAGGAAGCTTTATCTTCAAGATA  
ACCACATCAATCGGGTGCCCCAAATGCTTTTTCTTATCTAAGGCAGCTCTATCGACTGGATA  
TGTCCAATAATAACCTAAGTAATTTACCTCAGGGTATCTTTGATGATTTGGACAATATAACAC  
AACTGATTCTTCGCAACAATCCCTGGTATTGCGGGTGCAAGATGAAATGGGTACGTGACTGGT  
TACAATCACTACCTGTGAAGGTCAACGTGCGTGGGCTCATGTGCCAAGCCCCAGAAAAGGTTCT  
GTGGGATGGCTATTAAGGATCTCAATGCAGAACTGTTTGATTGTAAGGACAGTGGGATTGTAA  
GCACCATTCAGATAACCACTGCAATACCCAACACAGTGTATCCTGCCAAGGACAGTGGCCAG  
CTCCAGTGACCAAACAGCCAGATATTAAGAACCCCAAGCTCACTAAGGATCAACAAACCACAG  
GGAGTCCCTCAAGAAAAACAATTACAATTACTGTGAAGTCTGTACCTCTGATACCATTTCATA  
TCTCTTGAAACTTGCTCTACCTATGACTGCTTTGAGACTCAGCTGGCTTAACTGGGCCATA  
GCCCCGCATTTGGATCTATAACAGAAACAATTGTAACAGGGGAACGCAGTGAGTACTTGGTCA  
CAGCCCTGGAGCCTGATTCACCCTATAAAGTATGCATGGTTCCCATGGAAACCAGCAACCTCT  
ACCTATTTGATGAACTCCTGTTTGTATTGAGACTGAACTGCACCCCTTCGAATGTACAACC  
CTACAACCACCCTCAATCGAGAGCAAGAGAAAGAACCTTACAAAACCCCAATTTACCTTTGG  
CTGCCATCATTGGTGGGGCTGTGGCCCTGGTTACCATTGCCCTTCTTGCTTTAGTGTGTTGGT  
ATGTTTCATAGGAATGGATCGCTCTTCTCAAGGAAGTGTGCATATAGCAAAGGGAGGAGAAGAA  
AGGATGACTATGCAGAAGCTGGCACTAAGAAGGACAACCTCTATCCTGGAAATCAGGGAACTT  
CTTTTCAGATGTTACCAATAAGCAATGAACCCATCTCGAAGGAGGAGTTTGTAAATACACACCA  
TATTTCCCTAATGGAATGAATCTGTACAAAACAATCACAGTGAAAGCAGTAGTAACCGAA  
GCTACAGAGACAGTGGTATTCCAGACTCAGATCACTCACACTCATGATGCTGAAGGACTCACA  
GCAGACTTGTGTTTTGGGTTTTTTAAACCTAAGGGAGGTGATGGT

388/615

**FIGURE 384**

MISAAWSIFLIGTKIGLFLQVAPLSVMAKSCPSVCRCDAGFIYCNDRFLTSIPTGIPEDATTL  
YLQNNQINNAGIPSDLKNLLKVERIYLYHNSLDEFPTNLPKYVKELHLQENNIRTITYDSLK  
IPYLEELHLDDNSVSAVSIEEGAFRDSNYLRLLFLSRNHLSTIPWGLPRTIEELRLDDNRIST  
ISSPSLQGLTSLKRLVLDGNLLNNHGLGDKVFFNLVNLTELSLVRNSLTAAPVNLPGTNLRKL  
YLQDNHINRVPPNAFSYLRQLYRLDMSNNNLSNLPQGIFDDLDNITQLILRNNPWYCGCKMKW  
VRDWLQSLPVKVNVRGLMCQAPEKVRGMAIKDLNAELFDCKDSGIVSTIQITTAIPNTVYPAQ  
GQWPAPVTKQPDIKNPKLTKDQQTGSPSRKTITITVKSVTSDTIHISWKLALPMTALRLSWL  
KLGHSPAFGSITETIVTGERSEYLVTALEPDSPYKVCMPMETSNLYLFDETPVCJETETAPL  
RMYNPTTTLNREQEKEPYKNPNPLAAIIGGAVALVTIALLALVCWYVHRNGSLFSRNCAYSK  
GRRRKDDYAEAGTKKDNSILEIRETSFQMLPISNEPISKEEFVIHTIFPPNGMNLYKNNHSES  
SSNRSYRDSGIPDSDHSHS

**Important features of the protein:****Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 531-552

**N-glycosylation sites.**

amino acids 226-229, 282-285, 296-299, 555-558, 626-629, 633-636

**Tyrosine kinase phosphorylation site.**

amino acids 515-522

**N-myristoylation sites.**amino acids 12-17, 172-177, 208-213, 359-364, 534-539, 556-561,  
640-645**Amidation site.**

amino acids 567-570

**Leucine zipper pattern.**

amino acids 159-180

**Phospholipase A2 aspartic acid active site.**

amino acids 34-44

389/615

**FIGURE 385**

CCGTCATCCCCCTGCAGCCACCCTTCCCAGAGTCCTTTGCCCAGGCCACCCCAGGCTTCTTGG  
CAGCCCTGCCGGGCCACTTGTCTTCA**ATG**TCTGCCAGGGGGAGGTGGGAAGGAGGTGGGAGGAG  
GGCGTGACAGAGGCAGTCTGGGCTTGCCAGAGCTCAGGGTGCTGAGCGTGTGACCAGCAGTGA  
GCAGAGGCCCGCCATGGCCAGCCTGGGGCTGCTGCTCCTGCTCTTACTGACAGCACTGCCACC  
GCTGTGGTCCTCCTCACTGCCTGGGCTGGACACTGCTGAAAGTAAAGCCACCATTGCAGACCT  
GATCCTGTCTGCGCTGGAGAGAGCCACCGTCTTCTAGAACAGAGGCTGCCTGAAATCAACCT  
GGATGGCATGGTGGGGGTCCGAGTGCTGGAAGAGCAGCTAAAAAGTGTCCGGGAGAAGTGGGC  
CCAGGAGCCCCCTGCTGCAGCCGCTGAGCCTGCGCGTGCGGGATGCTGGGGGAGAAGCTGGAGGC  
TGCCATCCAGAGATCCCTCCACTACCTCAAGCTGAGTGATCCCAAGTACCTAAGAGAGTTCCA  
GCTGACCCTCCAGCCCCGGGTTTTTGAAGCTCCACATGCCTGGATCCACACTGATGCCTCCTT  
GGTGTACCCACGTTTCGGGCCCCAGGACTCATTCTCAGAGGAGAGAAGTGACGTGTGCCTGGT  
GCAGCTGCTGGGAACCGGGACGGACAGCAGCGAGCCCTGCGGCCTCTCAGACCTCTGCAGGAG  
CCTCATGACCAAGCCCCGGCTGCTCAGGCTACTGCCTGTCCCACCAACTGCTCTTCTCCTCTG  
GGCCAGAATGAGGGGATGCACACAGGGACCACTCCAACAGAGGCCAGGACTATATCAACCTCTT  
CTGCGCCAACATGATGGACTTGAACCGCAGAGCTGAGGCCATCGGATACGCCTACCCCTACCCG  
GGACATCTTCATGGAAAAATCATGTCTGTGGAATGGGCGGCTTCTCCGACTTCTACAAGCT  
CCGGTGGCTGGAGGCCATTCTCAGCTGGCAGAAACAGCAGGAAGGATGCTTCGGGGAGCCTGA  
TGCTGAAGATGAAGAATTATCTAAAGCTATTCAATATCAGCAGCATTTTTTCGAGGAGAGTGAA  
GAGGCGAGAAAAACAATTTCCAGATTCTCGCTCTGTTGCTCAGGCTGGAGTACAGTGGCGCAA  
TCTCGGCTCACTGCAACCTTTGCCTCCTGGGTTCAAGCAATTCTCTTGCTCATCCTCCCGAG  
TAGCTGGGACTACAGGAGCGTGCCACCATACTGGCTAATTTTTTATATTTTTTTAGTAGAGAC  
AGGGTTTTCATCATGTTGCTCATGCTGGTCTCGAACTCCTGATCTCAAGAGATCCGCCCACCTC  
AGGCTCCCAAAGTGTGGGATTAT**AGG**TGTGAGCCACCGTGTCTGGCTGAAAAGCACTTTCAAA  
GAGACTGTGTTGAATAAAGGGCCAAGGTTCTTGCCACCCAGCACTCATGGGGGCTCTCTCCCC  
TAGATGGCTGCTCCTCCCACAACACAGCCACAGCAGTGGCAGCCCTGGGTGGCTTCTTATACA  
TCCTGGCAGAATACCCCCCAGCAAACAGAGAGCCACACCCATCCACACCGCCACCACCAAGCA  
GCCGCTGAGACGGACGGTTCATGCCAGCTGCCTGGAGGAGGAACAGACCCCTTTAGTCCTCA  
TCCCTTAGATCCTGGAGGGCACGGATCACATCCTGGGAAGAAGGCATCTGGAGGATAAGCAAA  
GCCACCCCGACACCCAATCTTGGAAGCCCTGAGTAGGCAGGGCCAGGGTAGGTGGGGGCCGGG  
AGGGACCCAGGTGTGAACGGATGAATAAAGTTCAACTGCAACTGAAAAAAAAAAAA

390/615

**FIGURE 386**

MSARGRWEGGGRRACRGS LGLARAQGAERTVSSEQRPAMASLG LLLLLLLLTALPPLWSSSLPG  
LDTAESKATIADLILSALERATVFLEQRLPEINLDGMVGVRVLEEQLKSVREKWAQEPLLQPL  
SLRVGMLGEKLEAAIQ RSLHYLKLSDPKYLREFQLTLQPGFWKLPHAWIHTDASLVYPTFGPO  
DSFSEERSDVCLVQLLGTGTDSS EPCGLSDLCRSLMTKPGCSGYCLSHQLLFFLWARMRGCTQ  
GPLQQSQDYINLFCANMMDLNRRAE AIGYAYPTRDIFMENIMFCGMGGFSDFYKLRWLEAILS  
WQKQQEGCGFGE PD AEDEELSKAIQYQQHFSRRVKRREKQFPDSRSVAQAGVQWRNLGSLQPLP  
PGFKQFSC LILPSSWDYRSVPPYLANFYIFLVETGFHHVAHAGLELLISRPPTSGSQSVGL

**Important features of the protein:**

**Signal peptide:**

amino acids 1-26

**Transmembrane domain:**

amino acids 39-56

**Tyrosine kinase phosphorylation sites.**

amino acids 149-156, 274-282

**N-myristoylation sites.**

amino acids 10-16, 20-26, 63-69, 208-214

**Amidation site.**

amino acids 10-14

**Glycoprotein hormones beta chain signature 1.**

amino acids 230-237

391/615

**FIGURE 387**

GGTCTGAGTGCAGAGCTGCTGTC**ATG**GGCGGCCGCTCTGTGGGGCTTCTTTCCCGTCCTGCTGC  
TGCTGCTGCTATCGGGGGATGTCCAGAGCTCGGAGGTGCCCGGGGCTGCTGCTGAGGGATCGG  
GAGGGAGTGGGGTCGGCATAGGAGATCGCTTCAAGATTGAGGGGCGTGCAGTTGTTCCAGGGG  
TGAAGCCTCAGGACTGGATCTCGGCGGCCCGAGTGCTGGTAGACGGAGAAGAGCACGTCGGTT  
TCCTTAAGACAGATGGGAGTTTTGTGGTTCATGATATACCTTCTGGATCTTATGTAGTGGAAG  
TTGTATCTCCAGCTTACAGATTTGATCCCGTTCGAGTGGATATCACTTCGAAAGGAAAAATGA  
GAGCAAGATATGTGAATTACATCAAAACATCAGAGGTTGTCAGACTGCCCTATCCTCTCCAAA  
TGAAATCTTCAGGTCCACCTTCTTACTTTATTAAAAGGGAATCGTGGGGCTGGACAGACTTTC  
TAATGAACCCAATGGTTATGATGATGGTTCTTCCTTTATTGATATTTGTGCTTCTGCCTAAAG  
TGGTCAACACAAGTGATCCTGACATGAGACGGGAAATGGAGCAGTCAATGAATATGCTGAATT  
CCAACCATGAGTTGCCTGATGTTTCTGAGTTCATGACAAGACTCTTCTCTTCAAATCATCTG  
GCAAATCTAGCAGCGGCAGCAGTAAACAGGCAAAAGTGGGGCTGGCAAAGGAGG**TAG**TCAG  
GCCGTCCAGAGCTGGCATTGTCACAAACACGGCAACACTGGGTGGCATCCAAGTCTTGGA  
CCGTGTGAAGCAACTACTATAAACTTGAGTCATCCCGACGTTGATCTCTTACAACGTGTATGTT  
AACTTTTTAGCACATGTTTTGTACTTGGTACACGAGAAAACCCAGCTTTCATCTTTTGTCTGT  
ATGAGGTCAATATTGATGTCACTGAATTAATTACAGTGTCTATAGAAAATGCCATTAATAAA  
TTATATGAACTACTATACATTATGTATATTAATTAACATCTTAATCCAGAAATCAAAAAA  
AAAAAAAAAAAAAAAAAAAA

392/615

**FIGURE 388**

MAAALWGFFPVLLLLLLLLSGDVQSSEVPGAAAEAGSGSGVGIGDRFKIEGRAVVPGVKPDWIS  
AARVLVDGEEHVGFLLKTDGSFVVHDIPSGSYVVEVVSAPAYRFDVVRVDITSKGKMRARYVNYI  
KTSEVVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMLVPLLI FVLLPKVVNTSDPD  
MRREMEQSMNMLNSNHELDPVSEFMTRLFSSKSSGKSSSGSSSKTGKSGAGKRR

**Important features of the protein:****Signal sequence:**

amino acids 1-23

**Transmembrane domain:**

amino acids 161-182

**N-glycosylation site.**

amino acids 184-187

**Glycosaminoglycan attachment sites.**

amino acids 37-40, 236-239

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 151-154

**N-myristoylation sites.**

amino acids 33-38, 36-41, 38-44, 229-234

**Amidation site.**

amino acids 238-241

**ATP/GTP-binding site motif A (P-loop).**

amino acids 229-236

393/615

**FIGURE 389**

GTCGTGTGCTTGGAGGAAGCCGCGGAACCCCCAGCGTCCGTCCTCC**ATG**GCGTGGAGCCTTGGGAG  
CTGGCTGGGTGGCTGCCTGCTGGTGTGAGCATTGGGAATGGTACCACCTCCCGAAAATGTCAG  
AATGAATTCTGTTAATTTCAAGAACATTCTACAGTGGGAGTCACCTGCTTTTGCCAAAGGGAA  
CCTGACTTTTACAGCTCAGTACCTAAGTTATAGGATATTCCAAGATAAATGCATGAATACTAC  
CTTGACGGAATGTGATTTCTCAAGTCTTTCCAAGTATGGTGACCACACCTTGAGAGTCAGGGC  
TGAATTTGCAGATGAGCATTGAGACTGGGTAAACATCACCTTCTGTCCTGTGGATGACACCAT  
TATTGGACCCCTGGAATGCAAGTAGAAGTACTTGCTGATTCTTTACATATGCGTTTCTTAGC  
CCCTAAAATTGAGAATGAATACGAACTTGGACTATGAAGAATGTGTATAACTCATGGACTTA  
TAATGTGCAATACTGGAAAAACGGTACTGATGAAAAGTTTCAAATTACTCCCCAGTATGACTT  
TGAGGTCCTCAGAAACCTGGAGCCATGGACAACTTATTGTGTTCAAGTTCGAGGGTTTCTTCC  
TGATCGGAACAAAGCTGGGGAATGGAGTGAGCCTGTCTGTGAGCAAACAACCCATGACGAAAC  
GGTCCCTCCTGGATGGTGGCCGTCATCCTCATGGCCTCGGTCTTCATGGTCTGCCTGGCACT  
CCTCGGCTGCTTCTCCTTGCTGGTGGCTTACAAGAAGACAAAGTACGCCTTCTCCCTAG  
GAATTCTCTTCCACAGCACCTGAAAGAGTTTTTGGGCCATCCTCATCATAACACACTTCTGTT  
TTTCTCCTTTCCATTGTGCGATGAGAATGATGTTTTTGACAAGCTAAGTGTATTGCAGAAGA  
CTCTGAGAGCGGCAAGCAGAATCCTGGTGACAGCTGCAGCCTCGGGACCCGCTGGGCAGGG  
GCCCCAAAGCT**TAG**GCTCTGAGAAGGAACACACTCGGCTGGGCACAGTGACGTACTCCATCTC  
ACATCTGCCTCAGTGAGGGATCAGGGCAGCAAACAAGGGCCAAGACCATCTGAGCCAGCCCCA  
CATCTAGAACTCCAGACCTGGACTTAGCCACCAGAGAGCTACATTTTAAAGGCTGTCTTGGA  
AAAATACTCCATTTGGGAACCTCACTGCCTTATAAAGGCTTTCATGATGTTTTCAGAAGTTGGC  
CACTGAGAGTGTAATTTTTCAGCCTTTTATATCACTAAAATAAGATCATGTTTTAATTGTGAGA  
AACAGGGCCGAGCACAGTGGCTCACGCCTGTAATACCAGCACCTTAGAGGTGAGGCAGGCGG  
ATCACTTGAGGTGAGGAGTTCAAGACCAGCCTGGCCAATATGGTGAAACCCAGTCTCTACTAA  
AAATACAAAAATTAGCTAGGCATGATGGCGCATGCCTATAATCCCAGCTACTCGAGTGCCTGA  
GGCAGGAGAATTGCATGAACCCGGGAGGAGGAGGAGGAGGTTGCAGTGAGCCGAGATAGCGGC  
ACTGCACTCCAGCCTGGGTGACAAAGTGAGACTCCATCTCAAAAAAAAAAAAAAAAAAATTGTG  
AGAAACAGAAATACTTAAATGAGGAATAAGAATGGAGATGTTACATCTGGTAGATGTAACAT  
TCTACCAGATTATGGATGGACTGATCTGAAAATCGACCTCAACTCAAGGGTGGTCAGCTCAAT  
GCTACACAGAGCACGGACTTTTGGATTCTTTCAGTACTTTGAATTTATTTTCTACCTATAT  
ATGTTTTATATGCTGCTGGTGTCCATTAAAGTTTTACTCTGTGTTGC



394/615

**FIGURE 390**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA83551
><subunit 1 of 1, 325 aa, 1 stop
><MW: 37011, pI: 5.09, NX(S/T): 4
MAWSLGSWLGGCLLVSALGMVPPPENVRMNSVNFKNILQWESPAFAKGNLTFTAQYLSYRIFQ
DKCMNTTLTECDFSSLSKYGDHTLRVRAEFADHSWVNITFCPVDDTIIGPPGMQVEVLADS
LHMRFLAPKIENEYETWTMKNVNSWTYNVQYWKNGTDEKFQITPQYDFEVLRLNLEPWTTYCV
QVRGFLPDRNKAGEWSEPVCETTHDETVPSSWMAVILMASVFMVCLALLGCFSLWCVYKKT
KYAFSPRNSLPQHLKEFLGHPHNTLLFFSFPLSDENDVFDKLSVIAEDSESGKQNPGDSCSL
GTPPGQGPQS
```

**Important features of the protein:****Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 222-245

**N-glycosylation sites.**

amino acids 49-53, 68-72, 102-106, 161-165

**N-myristoylation sites.**

amino acids 6-12, 316-322

395/615

**FIGURE 391**

CTGTGCAGCTCGAGGCTCCAGAGGCACACTCCAGAGAGAGCCAAGGTTCTGACGCG**ATG**AGGA  
AGCACCTGAGCTGGTGGTGGCTGGCCACTGTCTGCATGCTGCTCTTCAGCCACCTCTCTGCGG  
TCCAGACGAGGGGCATCAAGCACAGAATCAAGTGGAACCGGAAGGCCCTGCCAGCACTGCCC  
AGATCACTGAGGCCCAGGTGGCTGAGAACCGCCCGGGAGCCTTCATCAAGCAAGGCCGCAAGC  
TCGACATTGACTTCGGAGCCGAGGGCAACAGGTACTACGAGGCCAACTACTGGCAGTTCCCCG  
ATGGCATCCACTACAACGGCTGCTCTGAGGCTAATGTGACCAAGGAGGCATTTGTCACCGGCT  
GCATCAATGCCACCCAGGCGGGCGAACCAGGGGGAGTTCCAGAAGCCAGACAACAAGCTCCACC  
AGCAGGTGCTCTGGCGGCTGGTCCAGGAGCTCTGCTCCCTCAAGCATTGCGAGTTTTGGTTGG  
AGAGGGGCGCAGGACTTCGGGTCACCATGCACCAGCCAGTGCTCCTCTGCCTTCTGGCTTTGA  
TCTGGCTCATGGTGAAAT**TAA**GCTTGCCAGGAGGCTGGCAGTACAGAGCGCAGCAGCGAGCAAA  
TCCTGGCAAGTGACCCAGCTCTTCTCCCCAAACCCACGCGTGTTCTGAAGGTGCCAGGAGC  
GGCGATGCACTCGCACTGCAAATGCCGCTCCACGTATGCGCCCTGGTATGTGCCTGCGTTCT  
GATAGATGGGGGACTGTGGCTTCTCCGTCACCTCCATTCTCAGCCCCTAGCAGAGCGTCTGGCA  
CACTAGATTAGTAGTAAATGCTTGATGAGAAGAACACATCAGGCACTGCGCCACCTGCTTCAC  
AGTACTTCCCAACAACCTCTTAGAGGTAGGTGTATTCCCGTTTTACAGATAAGGAACTGAGGC  
CCAGAGAGCTGAAGTACTGCACCCAGCATCACCAGCTAGAAAGTGGCAGAGCCAGGATTCAAC  
CCTGGCTTGTCTAACCCAGGTTTTCTGCTCTGTCCAATTCCAGAGCTGTCTGGTGATCACTT  
TATGTCTCACAGGGACCCACATCCAAACATGTATCTCTAATGAAATTGTGAAAGCTCCATGTT  
TAGAAATAAATGAAAACACCTGA

396/615

## **FIGURE 392**

MRKHL S W W L A T V C M L L F S H L S A V Q T R G I K H R I K W N R K A L P S T A Q I T E A Q V A E N R P G A F I K Q G  
R K L D I D F G A E G N R Y Y E A N Y W Q F P D G I H Y N G C S E A N V T K E A F V T G C I N A T Q A A N Q G E F Q K P D N K  
L H Q Q V L W R L V Q E L C S L K H C E F W L E R G A G L R V T M H Q P V L L C L L A L I W L M V K

**Important features of the protein:**

**Signal peptide:**

amino acids 1-26

**Transmembrane domain:**

amino acids 157-171

**N-glycosylation sites.**

amino acids 98-102, 110-114

**Tyrosine kinase phosphorylation site.**

amino acids 76-83

**N-myristoylation sites.**

amino acids 71-77, 88-94, 93-99, 107-113, 154-160

**Amidation site.**

amino acids 62-66

397/615

**FIGURE 393**

TGAAATGACTTCCACGGCTGGGACGGGAACCTTCCACCCACAGCTATGCCTCTGATTGGTGAA  
TGGTGAAGGTGCCTGTCTAACTTTTCTGTAAAAAGAACCAGCTGCCTCCAGGCAGCCAGCCCT  
CAAGCATCACTTACAGGACCAGAGGGACAAGACATGACTGTGATGAGGAGCTGCTTTTCGCCAA  
TTTAACACCAAGAAGAATTGAGGCTGCTTGGGAGGAAGGCCAGGAGGAACACGAGACTGAGAG  
**ATGA**ATTTTCAACAGAGGCTGCAAAGCCTGTGGACTTTAGCCAGACCCTTCTGCCCTCCTTTG  
CTGGCGACAGCCTCTCAAATGCAGATGGTTGTGCTCCCTTGCCCTGGGTTTTACCCTGCTTCTC  
TGGAGCCAGGTATCAGGGGCCCAGGGCCAAGAATTCACCTTTGGGCCCTGCCAAGTGAAGGGG  
GTTGTTCCCCAGAACTGTGGGAAGCCTTCTGGGCTGTGAAAGACACTATGCAAGCTCAGGAT  
AACATCACGAGTGCCCGGCTGCTGCAGCAGGAGGTTCTGCAGAACGTCTCGGATGCTGAGAGC  
TGTTACCTTGTCACACCCCTGCTGGAGTTCTACTTGAAAAGTGTTTTCAAAAACCACCACAAT  
AGAACAGTTGAAGTCAGGACTCTGAAGTCATTCTCTACTCTGGCCAACAAGTTGTTCTCATC  
GTGTCACAAGTGAACCCAGTCAAGAAAATGAGATGTTTTCCATCAGAGACAGTGCACACAGG  
CGGTTTCTGCTATTCCGGAGAGCATTCAAACAGTTGGACGTAGAAGCAGCTCTGACCAAAGCC  
CTTGGGGAAGTGGACATTCTTCTGACCTGGATGCAGAAATTCTACAAGCTCT**GA**ATGTCTAGA  
CCAGGACCTCCCTCCCCCTGGCACTGGTTTGTTCCTGTGTCAATTTCAAACAGTCTCCCTTCC  
TATGCTGTTCACTGGACACTTCACGCCCTTGGCCATGGGTCCCATTCTTGGCCCAGGATTATT  
GTCAAAGAAGTCATTCTTTAAGCAGCGCCAGTGACAGTCAGGGAAGGTGCCTCTGGATGCTGT  
GAAGAGTCTACAGAGAAGATTCTTGTATTTATTACAAGTCTATTTAATTAATGTCAGTATTTT  
AACTGAAGTTCTATTTATTTGTGAGACTGTAAGTTACATGAAGGCAGCAGAATATTGTGCCCC  
ATGCTTCTTTACCCCTCACAACTCCTTGCCACAGTGTGGGGCAGTGGATGGGTGCTTAGTAAGT  
ACTTAATAAACTGTGGTGCTTTTTTTGGCCTGTCTTTGGATTGTTAAAAACAGAGAGGGATG  
CTTGGATGTAAAGTGAAGTTCAGAGCATGAAAATCACACTGTCTTCTGATATCTGCAGGGAC  
AGAGCATTGGGGTGGGGGTAAAGGTGCATCTGTTTGAAGTAAACGATAAAATGTGGATTAA  
GTGCCCAGCACAAAGCAGATCCTCAATAAACATTTTCAATTTCCACCCACACTCGCCAGCTCAC  
CCCATCATCCCTTTCCCTTGGTGCCCTCCTTTTTTTTTTTATCCTAGTCATTCTTCCCTAATCT  
TCCACTTGAGTGTCAAGCTGACCTTGCTGATGGTGACATTGCACCTGGATGTACTATCCAATC  
TGTGATGACATTCCCTGCTAATAAAAGACAACATAACTCCAAAAAAAAAAAAAAAAAAAAA  
AAAA

398/615

**FIGURE 394**

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA88002
><subunit 1 of 1, 206 aa, 1 stop
><MW: 23799, pI: 9.12, NX(S/T): 3
MNFQQRLQSLWTLARPFPCPLLATASQMOMVVLPCLGFTLLLWSQVSGAQGQEFHFGPCQVKG
VVPQKLWEAFWAVKDTMQAQDNITSARLLQQEVLQNVSDAESCYLEVHTLLEFYLKTVFKNHHN
RTVEVRTLKSFSTLANNFVLIVSQLQPSQENEMFSIRDSAHRRFLLFRRAFKQLDVEAALTKA
LGEVDILLTWMQKFYKL
```

**Signal sequence:**  
amino acids 1-42

**N-glycosylation sites.**  
amino acids 85-89, 99-103, 126-130

399/615

**FIGURE 395**

GCCTTGGCCTCCCAAAGGGCTGGGATTATAGGCGTGACCACCATGTCTGGTCCAGAGTCTCAT  
TTCCTGATGATTTATAGACTCAAAGAAAACTATGTTCAGAAGCTCTCTTCTCTTCTGGCCTC  
CTCTCTGTCTTCTTTCCCTCTTTCTTCTTATTTTAATTAGTAGCATCTACTCAGAGTCATGCA  
AGCTGGAAATCTTTCATTTTGCTTGTCACTGGGGTAGGTCAGTCTTAGTTTTATTTTT  
TGAAATTTCACTTTCAGATTCAGGGGGTACATGTGAAGGTTTGTTTTATGAGTATATTGCAT  
GATGCTGAGGTTTGGGGT

400/615

**FIGURE 396**

MFRSSLLFWPPLCLLSLFLILISSIYSESKLEIFHFACQWGRSLSLSFYFLKFQLSDSGGT  
CEGLFYEYIA

**Important features of the protein:**

**Signal peptide:**

amino acids 1-25

**N-myristoylation site.**

amino acids 62-68

401/615

**FIGURE 397**

**CATG**CCGCTGCCGCCGCTGCTGCTGTTGCTCCTGGCGGCGCCTTGGGGACGGGCAGTTCCCTG  
TGTCTCTGGTGGTTTGCCTAAACCTGCAAACATCACCTTCTTATCCATCAACATGAAGAATGT  
CCTACAATGGACTCCACCAGAGGGTCTTCAAGGAGTTAAAGTTACTTACACTGTGCAGTATTT  
CATATATGGGCAAAAGAAATGGCTGAATAAATCAGAATGCAGAAATATCAATAGAACCTACTG  
TGATCTTTCTGCTGAAACTTCTGACTACGAACACCAGTATTATGCCAAAGTTAAGGCCATTTG  
GGGAACAAAGTGTTCCAAATGGGCTGAAAGTGACGGTTCTATCCTTTTTTTAGAAACACAAAT  
TGGCCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTTCTGTTGTCCTGACAGCTCC  
AGAGAAGTGGAAAGAGAAATCCAGAAGACCTTCCTGTTTCCATGCAACAAATATACTCCAATCT  
GAAGTATAACGTGTCTGTGTTGAATACTAAATCAAACAGAACGTGGTCCCAGTGTGTGACCAA  
CCACACGCTGGTGCTCACCTGGCTGGAGCCGAACACTCTTTACTGCGTACACGTGGAGTCCTT  
CGTCCCAGGGCCCCCTCGCCGTGCTCAGCCTTCTGAGAAGCAGTGTGCCAGGACTTTGAAAGA  
TCAATCATCAGAGTTCAAGGCTAAAATCATCTTCTGGTATGTTTTGCCCATATCTATTACCGT  
GTTTCTTTTTTCTGTGATGGGCTATTCCATCTACCGATATATCCACGTTGGCAAAGAGAAACA  
CCCAGCAAATTTGATTTTGATTTATGGAAATGAATTTGACAAAAGATTCTTTGTGCCTGCTGA  
AAAAATCGTGATTAACTTTATCACCTCAATATCTCGGATGATTCTAAAATTTCTCATCAGGA  
TATGAGTTTACTGGGAAAAAGCAGTGATGTATCCAGCCTTAATGATCCTCAGCCCAGCGGGAA  
CCTGAGGCCCCCTCAGGAGGAAGAGGAGGTGAAACATTTAGGGTATGCTTCGCATTTGATGGA  
AATTTTTTGTGACTCTGAAGAAAACACGGAAGGTACTTCTCTCAGGAGGAGGTGTCCACACAAGGAACATT  
ATTGGAGTCGCAGGCAGCGTTGGCAGTCTTGGGCCCGCAAACGTTACAGTACTCATACACCCC  
TCAGCTCCAAGACTTAGACCCCCTGGCGCAGGAGCACACAGACTCGGAGGAGGGGCCGGAGGA  
AGAGCCATCGACGACCCTGGTCGACTGGGATCCCCAACTGGCAGGCTGTGTATTCTTCGCT  
GTCCAGCTTCGACCAGGATTCAGAGGGCTGCGAGCCTTCTGAGGGGGATGGGCTCGGAGAGGA  
GGGTCTTCTATCTAGACTCTATGAGGAGCCGGCTCCAGACAGGCCACCAGGAGAAAATGAAAC  
CTATCTCATGCAATTCATGGAGGAATGGGGGTTATATGTGCAGATGGAAAAC**TGAT**GCCACA  
CTTCCTTTTGCCTTTTGTTCCTGTGCAAACAAGTGAGTCACCCCTTTGATCCCAGCCATAAA  
GTACCTGGGATGAAAGAAGTTTTTTCCAGTTTGTCAAGTGTCTGTGAGAA



402/615

**FIGURE 398**

MPLPPLLLLLLLAAPWGRAVPCVSGGLPKPANITFLSINMKNVLQWTPPEGLQGKVTYTVQYF  
IYGQKKWLNKSECRNINRTYCDLSAETSDYEHQYYAKVKAIWGTKCSKWAESGRFYPPFLETQI  
GPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQQIYSNLKYNVSVLNTKSNRTWSQCVTN  
HTLVLTWLEPNTLYCVHVESFVPGPPRAQPSEKQCARTLKDQSSEFKAKIIFWYVLPISITV  
FLFSVMGYSIYRYIHVGKEKHANLILYIGNEFDKRFFVPAEKIVINFITLNISSDDSKISHQD  
MSLLGKSSDVSSLNDPQPSGNLRPPQEEEEVKHLGYASHLMEIFCDSEENTEGTSLTQQESLS  
RTIPDPKTVIEYDYDVRTTDICAGPEEQELSLQEEVSTQGTLLSQALAVLGPQTLQYSYTP  
QLQDLDPPLAQEHTDSEEGPEEEPSTTLVDWDPQTGRLCIPSLSSFDQDSEGCEPSEGDLGEE  
GLLSRLYEPPAPDRPPGENETYLMQFMEEWGLYVQMEN

**Signal sequence:**

amino acids 1-18

**Transmembrane domain:**

amino acids 240-260

**N-glycosylation sites.**amino acids 31-34, 72-75, 80-83, 171-174, 180-183, 189-192,  
304-307, 523-526**Tyrosine kinase phosphorylation site.**

amino acids 385-392, 518-526

**N-myristoylation sites.**

amino acids 53-58, 106-111, 368-373, 492-497

**Tissue factor**

amino acids 1-278

403/615

**FIGURE 399**

CCGGCGATGTCGCTCGTGCTGCTAAGCCTGGCCGCGCTGTGCAGGAGCGCCGTACCCCGAGAG  
CCGACCGTTCAATGTGGCTCTGAAACTGGGCCATCTCCAGAGTGGATGCTACAACATGATCTA  
ATCCCCGAGACTTGAGGGACCTCCGAGTAGAACCTGTTACAACACTAGTGTGCAACAGGGGAC  
TATTCAATTTTGTGATGAATGTAAGCTGGGTACTCCGGGCAGATGCCAGCATCCGCTTGTGTAAG  
GCCACCAAGATTTGTGTGACGGGCAAAAGCAACTTCCAGTCCTACAGCTGTGTGAGGTGCAAT  
TACACAGAGGCCTTCCAGACTCAGACCAGACCCTCTGGTGGTAAATGGACATTTTCTTACATC  
GGCTTCCCTGTAGAGCTGAACACAGTCTATTTTATTGGGGCCCATAATATTCCTAATGCAAAT  
ATGAATGAAGATGGCCCTTCCATGTCTGTGAATTTACCTCACCAGGCTGCCTAGACCACATA  
ATGAAATATAAAAAAAGTGTGTCAAGGCCGGAAGCCTGTGGGATCCGAACATCACTGCTTGT  
AAGAAGAATGAGGAGACAGTAGAAGTGAACCTTCAACAACACTCCCCTGGGAAACAGATACATG  
GCTCTTATCCAACACAGCACTATCATCGGGTTTCTCAGGTGTTTGAGCCACACCAGAAGAAA  
CAAACGCGAGCTTCAGTGGTGATTCCAGTGACTGGGGATAGTGAAGGTGCTACGGTGCAGCTG  
ACTCCATATTTTCTTACTTGTGGCAGCGACTGCATCCGACATAAAGGAACAGTTGTGCTCTGC  
CCACAAACAGGCGTCCCTTTCCCTCTGGATAACAACAAAAGCAAGCCGGGAGGCTGGCTGCCT  
CTCCTCCTGCTGTCTCTGCTGGTGGCCACATGGGTGCTGGTGGCAGGGATCTATCTAATGTGG  
AGGCACGAAAGGATCAAGAAGACTTCCTTTTCTACCACCACACTACTGCCCCCATTAAGGTT  
CTTGTGGTTTACCCATCTGAAATATGTTTCCATCACACAATTTGTTACTTCACTGAATTTCTT  
CAAAACCATTCAGAAAGTGAGGTCACTCTTGAAGGTGGCAGAAAAAGAAAAATAGCAGAGATG  
GGTCCAGTGCAGTGGCTTGCCACTCAAAAGAAGGCAGCAGACAAAGTCGTCTTCCTTCTTTCC  
AATGACGTCAACAGTGTGTGCGATGGTACCTGTGGCAAGAGCGAGGGCAGTCCCAGTGAGAAC  
TCTCAAGACCTCTTCCCCCTTGCCCTTTAACCTTTTCTGCAGTGATCTAAGAAGCCAGATTCAT  
CTGCACAAATACGTGGTGGTCTACTTTAGAGAGATTGATACAAAAGACGATTACAATGCTCTC  
AGTGTCTGCCCCAAGTACCACCTCATGAAGGATGCCACTGCTTTCTGTGCAGAACTTCTCCAT  
GTCAAGCAGCAGGTGTCAGCAGGAAAAAGATCACAAAGCCTGCCACGATGGCTGCTGCTCCTTG  
**TAG**

404/615

**FIGURE 400**

MSLVLLSLAALCRSAVPREPTVQCGSETGPSPEWMLQHDLI PGDLRLDLRVEPVTTSVATGDYS  
ILMNVS WVL RADASIRLLKATKICVTGKS NFQSYSCVRCNYTEAFQTQTRPSGGKWTFSYIGF  
PVELNTVYFIGAHNIPNANMNEDGPSMSVNFTSPGCLDHIMKYKKKCVKAGSLWDPNITACKK  
NEETVEVNFTTTPLGNRYMALIQHSTIIGFSQVFEPHQKKQTRASVVIPVTGDSEGATVQLTP  
YFPTCGSDCIRHKGTVVLC PQTGV PFP L DNNKSKPGGWL P L L L L S L L V A T W V L V A G I Y L M W R H  
ERIKKTSFSTTTLLPPIKVLVVPSEICFHHTICYFTEFLQNHCRSEVILEKWQKKKIAEMGP  
VQWLATQKKAADKVVFLLSNDVNSVCDGTCGKSEGSPSENSQDLFPLAFNLFCSDLRSQIHLH  
KYVVVYFREIDTKDDYNALSVC PKYHLMKDATAFCAELLHV KQVSAGKRSQACHDGCCSL

**Important features of the protein:****Signal peptide:**

amino acids 1-14

**Transmembrane domain:**

amino acids 290-309

**N-glycosylation sites.**amino acids 67 - 71, 103 - 107, 156 - 160, 183 - 187, 197 - 201  
and 283 - 287**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 228 - 232 and 319 - 323

**Casein kinase II phosphorylation sites.**

amino acids 178 - 182, 402 - 406, 414 - 418 and 453 - 457

**N-myristoylation site.**

amino acids 116-122

**Amidation site.**

amino acids 488-452

405/615

**FIGURE 401**

GGGAACAGGGAACTATCAGCCCCTCGGCCCTCCGGGCCCTGCATTCTCTAGCCATGGACCG  
GGACCTTTTTGCGGCAGTCGCTAAATTGCCACGGGTCGTCTTTGCTCTCTCTACTTCGGAG  
CGAACAGCAGGACAATCCACACTTCCGTAGCCTCCTGGGGTCGGCCGCCGAGCCAGCCCCG  
GGGCCCCGCCGCCCCAGCACCCGTTGCAGGGCAGAAAAGAGAAGAGAGTTGACAACATCGA  
GATACAGAAATTCATCTCCAAAAAAGCGGATCTGCTTTTTGCACTTTCCTGGAAATCAGA  
TGCACCTGCAACTTCTGAAATTAATGAAGACAGTGAAGATCATTATGCAATCATGCCACC  
TTTAGAGCAATTCATGGAGATACCTAGTAGGATCGGAGAGAGCTGTTTTCCGAGATAT  
TGAGCGTGGTGATATAGTGATTGGAAGAATTAGTTCTATTCGGGAATTCGGTTTTTTCAT  
GGTGTTGATCTGTTTAGGAAGTGGTATCATGAGAGATATAGCCCACTTAGAAATCACAGC  
TCTTTGTCCCTTAAGAGATGTGCCTTCTCACAGTAACCATGGGGATCCTTTATCATATTA  
CCAAACTGGTGACATCATTTCGAGCTGGAATCAAGGATATTGACAGATACCATGAAAAGCT  
AGCAGTATCTCTGTATAGCTCTTCTCTCCACCACACCTATCTGGTATTAAATTAGGTGT  
AATTAGCTCTGAAGAGCTTCCTTTATACTACAGGAGAAGTGTTGAGCTAAATAGCAATTC  
TTTGGAGTCCTATGAAAATGTCATGCAGAGTTCCTTGGGATTTGTTAATCCAGGAGTAGT  
TGAATTCCTTCTAGAAAACTAGGAATAGATGAATCTAATCCACCATCTTTAATGAGAGG  
CCTACAAAGCAAAAATTTCTCTGAAGATGATTTTGCTTCTGCATTGAGAAAAAACAATC  
CGCATCTTGGGCTTTAAAATGTGTGAAGATCGGAGTTGACTATTTTAAAGTTGGACGCCA  
TGTGGATGCTATGAATGAATACAATAAAGCTTTGGAAATAGACAAACAAAACGTGGAAGC  
TTTGGTAGCTCGTGGAGCATTATATGCGACAAAAGGAAGTTTGAACAAAGCAATAGAAGA  
TTTTGAGCTTGCAATTAGAAAACGTCCAACCTCACAGAAATGCAAGAAAATACCTCTGCCA  
GACACTTGTAGAGAGAGGAGGACAGTTAGAAGAAGAAGAAAAGTTTTTAAATGCTGAAAG  
TTACTATAAGAAAGCCTTGGCTTTGGATGAGACTTTTAAAGATGCAGAGGATGCTTTGCA  
GAAACTTCATAAATATATGCAGAAATCTTTGGAATTAAGAGAAAAACAAGCTGAAAAGGA  
AGAAAAGCAGAAAACAAAGAAAATAGAAACAAGTGCAGAAAAGTTGCGTAAGCTCTTAAA  
AGAAGAGAAGAGGCTAAAGAAGAAAAGAAGAAAATCAACTTCTTCTTCAAGTGTTTCTTC  
TGCTGATGAATCAGTGTCTTCATCATCATCCTCTTCTCTCTGGTCACAAAAGGCATAA  
GAAACATAAGAGGAACCGTTCAGAGTCTTCTCGCAGTTCCAGAAGGCATTCATCTAGGGC  
ATCCTCAAATCAGATAGATCAGAATAGGAAAGATGAGTGCTACCCAGTTCAGCTAATAC  
TTCAGCATCTTTTCTTAACCATAAACAAGAAGTGGAGAACTACTGGGGAAGCAGGATAG  
GTTACAGTATGAAAAGACACAGATAAAAGAGAAAGATAGATGCCCTCTCTCTTCATCTTC  
ACTTGAAATACCGGATGATTTTGGAGTGTACTCCTATTTATTTAAAAAGTTAACTATAAA  
ACAGCCTCAGGCAGGTCCTTCAGGAGATATTCCAGAAGAGGGCATTGTTATCATAGATGA  
CAGCTCCATTCATGTTACTGACCCTGAAGACCTTCAAGTGGGACAAGATATGGAGGTGGA  
AGACAGTGGTATTGATGATCCTGACCACGGGTAGGCTTAGGTTTATGTGTGTGTATGTGT  
CTTAGTTTTTAACAAAAAAATTAAAAAGTAAAAAACTAAAAATAGAAAAATGCTTAGAG  
AATAAGGATATAAAGAATATTTTTGTGCAGTTGAACAATGAGTGCTTAAGCTAAATGTCA  
TCACAAAAGAGTAAAAAAATTTTACAAAATTAAAAATGTTTAAAGTTAAAAAGCTCTAGG  
AAGCTAAGGTCAATTTATTATTGGAGAAATAAAATTATTTTATGAATTACTGT

406/615

**FIGURE 402**

MDRDLRLQSLNCHGSSLLSLLRSEQQDNPHFRSLLGSAAEPARGPPPPQHPLQGRKEKRVD  
NIEIQKFISKKADLLFALSWKSDAPATSEINEDSEDHYAIMPPLEQFMEIPSMRRELFF  
RDIERGDIVIGRISSIREFGFFMVLICLGSGIMRDIAHLEITALCPLRDVPSHSNHGDPL  
SYYQTGDIIRAGIKDIDRYHEKLAVSLYSSSLPPLHSGIKLGVISSEELPLYRRSVELN  
SNSLESYENVMQSSLGFVNPGVVEFLLEKLGIDESNPPSLMRGLQSKNFSEDDFASALRK  
KQSASWALKCVKIGVDYFKVGRHVDAMNEYNKALEIDKQNVREALVARGALYATKGSLNKA  
IEDFELALENCPTHNRKYLQCTLVERGGQLEEEEEKFLNAESYYKKALALDETFFKDAED  
ALQKLHKYMQKSLELREKQAEKEEKQTKKIETSAEKLRLKLLKEEKRLKKRRKSTSSSS  
VSSADESVSSSSSSSSSGHKKRHHKRNRSSESSRRHSSRRASSNQIDQNRKDECYPVP  
ANTSASFLNHKQEVKLLGQDRLOQYEKTOIKEKDRCPLSSSSLEIPDDFGVYSYLFKKL  
TIKQPQAGPSGDIPEEGIVIIDDSSIHVTDPEDLQVGQDMEVEDSGIDDPDHG

**Important features of the protein:****Signal peptide:**

Amino acids 1-23

**Transmembrane domain:**

Amino acids 138-155

**N-glycosylation sites:**

Amino acids 288-292;508-512;542-546

**cAMP- and cGMP-dependent protein kinase phosphorylation sites:**

Amino acids 300-304;472-476;473-477;517-521;598-602

**N-myristoylation sites:**

Amino acids 218-224;222-228;271-277;348-354

**Amidation site:**

Amino acids 52-56

**Cell attachment sequence:**

Amino acids 125-128

407/615

**FIGURE 403**

CCGAGGCGGGAGGAGCCCGAGGGGGCGCGAGCCCCGCATGAATCATTGTAGTCAATCATTTTC  
CAGTTCTCAGCCGCTCAGTTGTGATCAAGGGACACGTGGTTTCCGAAGTCCAGCTCAGAATA  
GGAAAATAACTTGGGATTTTATATTGGAAGACATGGATCTTGCTGCCAACGAGATCAGCATTT  
ATGACAACTTTTCAGAGACTGTTGATTTGGTGAGACAGACCGGCCATCAGTGTGGCATGTCAG  
AGAAGGCAATTGAAAAATTTATCAGACAGCTGCTGGAAAAGAATGAACCTCAGAGACCCCCC  
CGCAGTATCCTCTCCTTATAGTTGTGTATAAGGTTCTCGCAACCTTGGGATTAATCTTGCTCA  
CTGCCTACTTTGTGATTCAACCTTTTCAGCCCATTAGCACCTGAGCCAGTGCTTTCTGGAGCTC  
ACACCTGGCGCTCACTCATCCATCACATTAGGCTGATGTCCTTGCCCATTGCCAAGAAGTACA  
TGTCAGAAAATAAGGGAGTTCTCTGCATGGGGGTGATGAAGACAGACCTTTCCAGACTTTG  
ACCCCTGGTGGACAAACGACTGTGAGCAGAATGAGTCAGAGCCCATTCTGCCAAGTGCAGTGT  
GCTGTGCCCAGAAACACCTGAAGGTGATGCTCCTGGAAGACGCCCCAAGGAAATTTGAGAGGC  
TCCATCCACTGGTGATCAAGACGGGAAAGCCCCCTGTTGGAGGAAGAGATTTCAGCATTTTTTGT  
GCCAGTACCCTGAGGCGACAGAAGGCTTCTCTGAAGGGTTTTTCGCAAGTGGTGGCGCTGCT  
TTCCTGAGCGGTGGTTCCCATTTCTTATCCATGGAGGAGACCTCTGAACAGATCACAAATGT  
TACGTGAGCTTTTTCTGTTTTCACTCACCTGCCATTTCCAAAAGATGCCTCTTTAAACAAGT  
GCTCCTTTCTTCACCCAGAACCTGTTGTGGGGAGTAAGATGCATAAGATGCCTGACCTATTTA  
TCATTGGCAGCGGTGAGGCCATGTTGCAGCTCATCCCTCCCTTCCAGTGCCGAAGACATTGTC  
AGTCTGTGGCCATGCCAATAGAGCCAGGGGATATCGGCTATGTCGACACCACCACTGGAAGG  
TCTACGTTATAGCCAGAGGGGTCCAGCCTTTGGTCATCTGCGATGGAACCGCTTTCTCAGAAC  
TGTAGGAAATAGAACTGTGCACAGGAACAGCTTCCAGAGCCGAAAACCAGGTTGAAAGGGGAA  
AAATAAAAACAAAAACGATGAAACTGCAAAA

408/615

**FIGURE 404**

MDLAANEISIIYDKLSETVDLVRQTGHQCGMSEKAIEKFIRQLLEKNEPQRPPPOYPLLIIVVYK  
VLATLGLILLTAYFVIQPFSPLAPEPVLSGAHTWRSLIHHIRLMSLPIAKKYMSENKGVPLHG  
GDEDRPFPDFDPWWTNDCEQNESEPI PANCTGCAQKHLKVMILLEDAPRKFERLHPLVIKTGKP  
LLEEEIQHFLCQYPEATEGFSEGFFAKWWRCFPERWFFFPYPWRRPLNRSQMLRELFVVFTHL  
PFPKDASLNKCSFLHPEPVVGSKMHKMPDLFIIGSGEAMLQLIPPFQRRHCQSVAMPIEPGD  
IGYVDTTHWKVYVIARGVQPLVICDGTAFSEL

409/615

**FIGURE 405**

TGCCGGGCTGCGGGGCGCCTTGACTCTCCCTCCACCCTGCCTCCTCGGGCTCCACTCGTCTGCCCCCTGGACTCCC  
GTCTCCTCCTGTCTCCGGCTTCCCAGAGCTCCCTCCTTATGGCAGCAGCTTCCCGCGTCTCCGGCGCAGCTTCT  
CAGCGGACGACCCCTCTCGCTCCGGGGCTGAGCCCAGTCCCTGGATGTTGCTGAAACTCTCGAGATCATGCGCGGG  
TTTGGCTGCTGCTTCCCCGCCGGGTGCCACTGCCACCGCCGCCCTCTGCTGCCGCCGTCCGCGGGATGCTCAG  
TAGCCCGCTGCCCGGCCCGCGATCCTGTGTTCTCGGAAGCCGTTTGCTGCTGCAGAGTTGCACGAACTAGTC  
ATGGTGCTGTGGGAGTCCCCGCGGCAGTGCAGCAGCTGGACACTTTGCGAGGGCTTTTGCTGGCTGCTGCTGCTG  
CCCGTCATGCTACTCATCGTAGCCCGCCCGGTGAAGCTCGCTGCTTCCCTACCTCCTTAAGTGACTGCCAAACG  
CCCACCGGCTGGAATTGCTCTGGTTATGATGACAGAGAAAATGATCTCTTCTCTGTGACACCAACACCTGTAAA  
TTTGATGGGGAATGTTTAAGAATTGGAGACACTGTGACTTGCGTCTGTCAAGTCAAGTCAACAATGACTATGTG  
CCTGTGTGTGGCTCCAATGGGGAGAGCTACCAGAATGAGTGTACCTGCGACAGGCTGCATGCAAACAGCAGAGT  
GAGATACTTGTGGTGTGAGAAGGATCATGTGCCACAGATGCAGGATCAGGATCTGGAGATGGAGTCCATGAAGGC  
TCTGGAGAACTAGTCAAAAGGAGACATCCACCTGTGATATTTGCCAGTTTGGTGCAGAATGTGACGAAGATGCC  
GAGGATGTCTGGTGTGTGTGTAATATTGACTGTTCTCAAACCAACTTCAATCCCCTCTGCGCTTCTGATGGGAAA  
TCTTATGATAATGCATGCCAAATCAAAGAAGCATCGTGTGAGAAACAGGAGAAAATTGAAGTCATGTCTTTGGGT  
CGATGTCAAGATAACACAACACTAAGTCTGAAGATGGGCATTATGCAAGAACAGATTATGCAGAGAAT  
GCTAACAAATTAGAAGAAAGTGCCAGAGAACACCACATACCTTGTCCGGAACATTACAATGGCTTCTGCATGCAT  
GGGAAGTGTGAGCATTCTATCAATATGCAGGAGCCATCTTGCAGGTGTGATGCTGTTATACTGGACAACACTGT  
GAAAAAAGGACTACAGTGTTCTATACGTTGTTCCCGGTCCTGTACGATTTCAAGTATGTCTTAATCGCAGCTGTG  
ATTGGAACAATTGAGATTGCTGTCTGTGTGGTGGTCCCTCTGCATCACAAGGAAATGCCCCAGAAGCAACAGA  
ATTACAGACAGAAGCAAAATACAGGGCACTACAGTTTACAGACAATACAACAAGAGCGTCCACGAGGTTAATCTAA  
AGGGAGCATGTTTACAGTGGCTGGACTACCGAGAGCTTGGACTACACAATACAGTATTATAGACAAAAGAATAA  
GACAAGAGATCTACACATGTTGCCTTGCAATTTGTGGTAATCTACACCAATGAAAACATGTACTACAGCTATATTT  
GATTATGTATGGATATATTTGAAATAGTATACATTGTCTTGATGTTTTTCTGTAATGTAAATAAACTATTTATA  
TCACACAATATAGTTTTTCTTTCCCATGTATTTGTTATATATAATAAATACTCAGTGATGAG



410/615

**FIGURE 406**

MVLWESPRQCSSWTLCEGFCWLLLLLPVMLLIVARPVKLAAFPTSLSDCQTPTGWNC SGY  
DDRENDLFLCDTNTCKFDGECLRIGDTVTCVCQFKCNDYVPVCGSNGESYQNECYLRQ  
AACKQQSEILVVSEGSCATDAGSGSGDGVHEGSGETSQKETSTCDICQFGAECDEDAED  
VWCVCNIDCSQTNFNPLCASDGKSYDNACQIKEASCQKQEKIEVMSLGRCQDNTTTT TK  
SEDGHYARTDYAENANKLEESAREHHIPCPEHYNGFCMHGKCEHSINMQEPSCRC DAGY  
TGQHCEKKDYSVLYVVPGPVRFQYVLIAAVIGTIQIAVICVVVLCITRKCPRSNRIHRQ  
KQNTGHYSSDNTTRASTRLI

411/615

**FIGURE 407**

CTCGCAGCCGAGCGCGGCCGGGAAGGGCTCTCCTTCCAGCGCCGAGCACTGGGCCCTGGCAG  
ACGCCCCAAGATTGTTGTGAGGAGTCTAGCCAGTTGGTGAGCGCTGTAATCTGAACCAGCTGT  
GTCCAGACTGAGGCCCCATTTGCATTGTTTAACTACTTAGAAAATGAAGTGTTCATTTTTAA  
CATTCCTCCTCCAATTGTTTAAATGCTGAATTACTGAAGAGGGCTAAGCAAAACCAGGTGCTT  
GCGCTGAGGGCTCTGCAGTGGCTGGGAGGACCCCGCGCTCTCCCGTGTCTCTCCACGACT  
CGCTCGGCCCTCTGGAATAAAACACCCGCGAGCCCCGAGGGCCCAGAGGAGGCCGACGTGCC  
CGAGCTCCTCCGGGGGTCCCGCCCGAGCTTTCTTCTCGCCTTCGCATCTCCTCCTCGCGCG  
TCTTGACATGCCAGGAATAAAAAGGATACTACTGTTACCATTCTGGCTCTCTGTCTTCCAA  
GCCCTGGGAATGCACAGGCACAGTGCACGAATGGCTTTGACCTGGATCGCCAGTCAGGACAGT  
GTTTAGATATTGATGAATGCCGAACCATCCCCGAGGCCTGCCGAGGAGACATGATGTGTGTTA  
ACCAAATGGCGGGTATTTATGCATTCCCCGGACAAACCCTGTGTATCGAGGGCCCTACTCGA  
ACCCCTACTCGACCCCTACTCAGGTCCGTACCCAGCAGCTGCCCCACCACTCTCAGCTCCAA  
ACTATCCACGATCTCCAGGCCTCTTATATGCCGCTTTGGATAACCAGATGGATGAAAGCAACC  
AATGTGTGGATGTGGACGAGTGTGCAACAGATTCCCACCAGTGCAACCCACCCAGATCTGCA  
TCAATACTGAAGGCGGGTACACCTGCTCCTGACCGACGGATATTGGCTTCTGGAAGGCCAGT  
GCTTAGACATTGATGAATGTGCTATGGTTACTGCGCAGCTCTGTGCGAATGTTCTTGAT  
CCTATTCTTGATACATGCAACCCTGGTTTTACCCTCAATGAGGATGGAAGCTCTTGCCAAGATG  
TGAACGAGTGTGCCACCGAGAACCCTGCGTGCAACCTGCGTCAACACCTACGGCTCTCTCA  
TCTGCCGCTGTGACCCAGGATATGAACTTGAGGAAGATGGCGTTTATTGCAGTATGGACG  
AGTGCAGCTTCTCTGAGTTCTCTGCCAACATGAGTGTGTGAACCAGCCCGGCACATACTTCT  
GCTCCTGCCCTCCAGGCTACATCCTGCTGGATGACAACCGAAGCTGCCAAGACATCAACGAAT  
GTGAGCACAGGAACACACAGTGCACCTGCAGCAGACGTGCTACAATTTACAAGGGGGCTTCA  
AATGCATCGACCCCATCCGCTGTGAGGAGCCTTATCTGAGGATCAGTGATAACCGCTGTATGT  
GTCCTGCTGAGAACCCTGGCTGCAGAGACCAGCCCTTTACCATCTTGTACCGGGACATGGACG  
TGGTGTGAGGACGCTCCGTTCCCGCTGACATCTTCCAAATGCAAGCCACGACCCGCTACCCTG  
GGGCCTATTACATTTTCCAGATCAAATCTGGGAATGAGGGCAGAGAATTTTACATGCGGCAAA  
CGGGCCCCATCAGTGCCACCCTGGTGATGACACGCCCCATCAAAGGGCCCCGGGAAATCCAGC  
TGGACTTGGAATGATCACTGTCAACACTGTCATCAACTTCAGAGGCAGCTCCGTGATCCGAC  
TGCGGATATATGTGTGCGAGTACCCATTCTGAGCCTCGGGCTGGAGCCTCCGACGCTGCCTCT  
CATTGGCACCAAGGGACAGGAGAAGAGAGGAATAACAGAGAGAATGAGAGCGACACAGACGT  
TAGGCATTTCTGCTGAACGTTTCCCCGAAGAGTCAGCCCCGACTTCCTGACTCTCACCTGTA  
CTATTGCAGACCTGTCACCCTGCAGGACTTGCCACCCCCAGTTCTTATGACACAGTTATCAAA  
AAGTATTATCATTGCTCCCCTGATAGAAGATTGTTGGTGAATTTTCAAGGCCTTCAGTTTATT  
TCCACTATTTTCAAAGAAAATAGATTAGGTTTGCGGGGTCTGAGTCTATGTTCAAAGACTGT  
GAACAGCTTGCTGTCACTTCTTACCTCTTCCACTCCTTCTCTCACTGTGTTACTGCTTTGCA  
AAGACCCGGGAGCTGGCGGGGAACCCTGGGAGTAGCTAGTTTGCTTTTTCGTACACAGAGAA  
GGCTATGTAAACAAACCACAGCAGGATCGAAGGGTTTTTAGAGAATGTGTTTCAAACCATGC  
CTGGTATTTTCAACCATAAAAGAAGTTTCAGTTGTCCTTAAATTTGTATAACGGTTTAATTCT  
GTCTTGTTTCAATTTGAGTATTTTAAAAAATATGTCGTAGAATTCCTTCGAAAGGCCTTCAGA  
CACATGCTATGTTCTGTCTTCCCAAACCCAGTCTCCTCTCCATTTTAGCCAGTGTTTTCTTT  
GAGGACCCCTTAATCTTGCTTTCTTTAGAATTTTACCCAATTGGATTGGAATGCAGAGGTCT  
CCAAACTGATTAAATATTTGAAGAGA

412/615

**FIGURE 408**

MPGIKRILTVTILALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGYPYSPYSTPYSGPYPAAAPPLSAPNYPTISRPLICRFGYQMDENQCVDVDECATDSHQCNPTQICINTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSGLICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPFITILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEMITVNTVINFRGSSVIRLRIYVSQYPF

**Important features of the protein:****Signal peptide:**

amino acids 1-25

**N-glycosylation sites.**

amino acids 283-287, 296-300

**N-myristoylation sites.**

amino acids 21-27, 64-70, 149-155, 186-192, 226-232, 242-248, 267-273, 310-316

**Aspartic acid and asparagine hydroxylation sites.**

amino acids 144-156, 181-193, 262-274

**Cell attachment sequence.**

amino acids 54-57

**Calcium-binding EGF-like.**

amino acids 131-166, 172-205, 211-245, 251-286

413/615

**FIGURE 409**

CCCACGCGTCCGCGGACGCGTGGGTGCGACTAGTTCTAGATCGCGAGCGGCCGCCCGCGGCTCA  
GGGAGGAGCACCGACTGCGCCGCACCCTGAGAGATGGTTGGTGCCATGTGGAAGGTGATTGTT  
TCGCTGGTCCTGTTGATGCCTGGCCCCTGTGATGGGCTGTTTCGCTCCCTATACAGAAGTGTT  
TCCATGCCACCTAAGGGAGACTCAGGACAGCCATTATTTCTCACCCTTACATTGAAGCTGGG  
AAGATCCAAAAAGGAAGAGAATTGAGTTTGGTCGGCCCTTTCCAGGACTGAACATGAAGAGT  
TATGCCGGCTTCCTCACCCTGAATAAGACTTACAACAGCAACCTCTTCTTCTGGTTCTTCCCA  
GCTCAGATACAGCCAGAAGATGCCCCAGTAGTTCTCTGGCTACAGGGTGGGCCGGGAGGTTCA  
TCCATGTTTGGACTCTTTGTGGAACATGGGCCTTATGTTGTCACAAGTAACATGACCTTGCGT  
GACAGAGACTTCCCCTGGACCACAACGCTCTCCATGCTTTACATTGACAATCCAGTGGGCACA  
GGCTTCAGTTTTTACTGATGATACCCACGGATATGCAGTCAATGAGGACGATGTAGCACGGGAT  
TTATACAGTGCACATAATTCAGTTTTTCCAGATATTTCTGAATATAAAAAATAATGACTTTTAT  
GTCAGTGGGGAGTCTTATGCAGGGAAATATGTGCCAGCCATTGCACACCTCATCCATTCCCTC  
AACCCTGTGAGAGAGGTGAAGATCAACCTGAACGGAATTGCTATTGGAGATGGATATTCTGAT  
CCCGAATCAATTATAGGGGGCTATGCAGAATTCCTGTACCAAATTGGCTTGTGGATGAGAAG  
CAAAAAAGTACTTCCAGAAGCAGTGCCATGAATGCATAGAACACATCAGGAAGCAGAACTGG  
TTTGAGGCCCTTTGAAATACTGGATAAACTACTAGATGGCGACTTAACAAGTGATCCTTCTTAC  
TTCCAGAATGTTACAGGATGTAGTAATTACTATAACTTTTTTGGGTTGCACGGAACCTGAGGAT  
CAGCTTTTACTATGTGAAATTTTTGTCACTCCCAGAGGTGAGACAAGCCATCCACGTGGGGAAT  
CAGACTTTTAAATGATGGAACATAGTTGAAAAGTACTTGGCGAGAAGATACAGTACAGTCAGTT  
AAGCCATGGTTAACTGAAATCATGAATAATTATAAGGTTCTGATCTACAATGGCCAACTGGAC  
ATCATCGTGGCAGCTGCCCTGACAGAGCGCTCCTTGATGGGCATGGACTGGAAAGGATCCCGAG  
GAATACAAGAAGGCAGAAAAAAAAGTTTGAAGATCTTTAAATCTGACAGTGAAGTGGCTGGT  
TACATCCGCAAGCGGGTGAATTCATCAGGTAATTATTGAGGTGGAGGACATATTTTACCC  
TATGACCAGCCTCTGAGAGCTTTTGACATGATTAATCGATTCAATTTATGGAAAAGGATGGGAT  
CCTTATGTTGGATTAATACTACCTTCCCAAAGAGAACATCAGAGGTTTTTATTGCTGAAAAGAA  
AATCGTAAAAACAGAAAATGTCATAGGAATAAAAAAATTATCTTTTCATATCTGCAAGATTTT  
TTTCATCAATAAAAAATTATCCTTGAAACAAGTGAGCTTTTGTGTTTTGGGGGAGATGTTTACT  
ACAAAATTAACATGAGTACATGAGTAAGAATTACATTATTTAACTTAAAGGATGAAAGGTATG  
GATGATGTGACACTGAGACAAGATGTATAAATGAAATTTTAGGGTCTTGAATAGGAAGTTTTA  
ATTTCTTCTAAGAGTAAGTGAAGGTGCAGTTGTAACAAACAAAGCTGTAACATCTTTTCTG  
CCAATAACAGAAGTTTGGCATGCCGTGAAGGTGTTTGGAAATATTATTGGATAAGAATAGCTC  
AATTATCCCAAATAAATGGATGAAGCTATAATAGTTTTGGGGAAAAGATTCTCAAATGTATAA  
AGTCTTAGAACAAAAGAATTCTTTGAAATAAAAAATATTATATATAAAAGTAAAAA

414/615

**FIGURE 410**

MVGAMWKVIVSLVLLMPGPGCDGLFRSLYRSVSMPPKGDGSGQPLFLTPYIEAGKIQKGRELSLV  
GPFPGNLNMKSYAGFLT VNKTYNSNLFFWFPAQIQPEDAPVVLWLQGGPGGSSMFGLFVEHGP  
YVVT SNMTLRDRDFPWT T T L S M L Y I D N P V G T G F S F T D D T H G Y A V N E D D V A R D L Y S A L I Q F F Q I  
FPEYKNNDFYVTGESYAGKYVPAIAHLIHS LN P V R E V K I N L N G I A I G D G Y S D P E S I I G G Y A E F  
LYQIGLLDEKQKKYFQKQCHECIEHIRKQNWFEAFEILDKLLDGLTSDPSYFQNV TGCSNYY  
NFLRCTEPEDQLYYVKFLSLPEVRQAIHVG N Q T F N D G T I V E K Y L R E D T V Q S V K P W L T E I M N N Y  
KVLIYNGQLDII V A A A L T E R S L M G M D W K G S Q E Y K K A E K K V W K I F K S D S E V A G Y I R Q A G D F H Q V  
IIRGGGHILPYDQPLRAFDMINRFIYKGWD PYVG

**Signal sequence:**

amino acids 1-22

**N-glycosylation site.**

amino acids 81-85, 132-136, 307-311, 346-350

**Casein kinase II phosphorylation site.**amino acids 134-138, 160-164, 240-244, 321-325, 334-338, 348-352,  
353-357, 424-428**Tyrosine kinase phosphorylation site.**

amino acids 423-432

**N-myristoylation site.**

amino acids 22-28, 110-116, 156-162, 232-238

**Serine carboxypeptidases, serine active site.**

amino acids 200-208

**Crystallins beta and gamma 'Greek key' motif signature.**

amino acids 375-391

415/615

**FIGURE 411**

GCAAGCCAAGGCGCTGTTTGAGAAGGTGAAGAAGTTCGGACCCATGTGGAGGAGGGGGACATTGTGTACCGCCT  
CTACATGCGGCGAGACCATCATCAAGGTGATCAAGTTCATCCTCATCATCTGCTACACCGTCTACTACGTGCACAA  
CATCAAGTTCGACGTGGACTGCACCGTGGACATTGAGAGCCTGACGGGCTACCGCACCTACCGTGTGCCCCACCC  
CCTGGCCACACTCTTCAAGATCCTGGCGTCCCTCTACATCAGCCTAGTCATCTTCTACGGCCTCATCTGCATGTA  
CACACTGTGGTGGATGCTACGGCGCTCCCTCAAGAAGTACTCGTTTGAGTCGATCCGTGAGGAGAGCAGCTACAG  
CGACATCCCCGACGTCAAGAACGACTTCGCCTTCATGCTGCACCTCATTGACCAATACGACCCGCTCTACTCCAA  
GCGCTTCGCCGTCTTCTGTCGGAGGTGAGTGAGAACAAGCTGCGGCAGCTGAACCTCAACAACGAGTGGAGCCT  
GGACAAGCTCCGGCAGCGGCTCACCAAGAACGCGCAGGACAAGCTGGAGCTGCACCTGTTTCATGCTCAGTGGCAT  
CCCTGACACTGTGTTTGACCTGGTGGAGCTGGAGGTCTCAAGCTGGAGCTGATCCCCGACGTGACCATCCCCGCC  
CAGCATTGCCAGCTCACGGGCTCAAGGAGCTGTGGCTCTACCACACAGCGGCCAAGATTGAAGCGCCTGCGCT  
GGCCTTCTGCGCGAGAACCTGCGGGCGCTGCACATCAAGTTCACCGACATCAAGGAGATCCCGCTGTGGATCTA  
TAGCCTGAAGACACTGGAGGAGCTGCACCTGACGGGCAACCTGAGCGCGGAGAACAACCGCTACATCGTCATCGA  
CGGGCTGCGGGAGCTCAAACGCCTCAAGGTGCTGCGGCTCAAGAGCAACCTAAGCAAGCTGCCACAGGTGGTCAC  
AGATGTGGGCGTGCACCTGCAGAAGCTGTCCATCAACAATGAGGGCACCAAGCTCATCGTCTCAACAGCCTCAA  
GAAGATGGCGAACCTGACTGAGCTGGAGCTGATCCGCTGCGACCTGGAGCGCATCCCCACTCCATCTTCAGCCT  
CCACAACCTGCAGGAGATTGACCTCAAGGACAACAACCTCAAGACCATCGAGGAGATCATCAGCTTCAGCACCT  
GCACCGCTCAGCTGCCTTAAGCTGTGGTACAACCATCGCCTACATCCCCATCCAGATCGGCAACCTCACCAA  
CCTGGAGCGCCTCTACCTGAACCGCAACAAGATCGAGAAGATCCCCACCCAGCTCTTCTACTGCCGCAAGCTGCG  
CTACCTGGACCTCAGCCACAACAACCTGACCTTCCTCCCTGCGACATCGGCCTCCTGCAGAACCTCCAGAACCT  
AGCCATCACGGCCAACCGGATCGAGACGCTCCCTCCGGAGCTCTCCAGTGCCGGAAGCTGCGGGCCCTGCACCT  
GGGCAACAACGTGCTGCAGTCACTGCCCTCCAGGTGGGCGAGCTGACCAACCTGACGCAGATCGAGCTGCGGGG  
CAACCGGCTGGAGTGCTGCCTGTGGAGCTGGGCGAGTGCCACTGCTCAAGCGCAGCGGCTGGTGGTGGAGGA  
GGACCTGTTCAACACACTGCCACCCGAGGTGAAGGAGCGGCTGTGGAGGGCTGACAAGGAGCAGGCTGAGCGAG  
GCCGGCCCAGCACAGCAAGCAGCAGGACCGCTGCCAGTCTCAGGCCCGGAGGGGCGAGGCTAGCTTCTCCAG  
AACTCCCGGACAGCCAGGACAGCCTCGCGGCTGGGCGAGGCTGGGGCCGCTTGTGAGTCAGGCCAGAGCGAGA  
GGACAGTATCTGTGGGGCTGGCCCCCTTTCTCCCTCTGAGACTCACGTCCCCCAGGGCAAGTGCTTGTGGAGGAG  
AGCAAGTCTCAAGAGCGCAGTATTTGGATAATCAGGGTCTCCTCCCTGGAGGCCAGCTTGCCCCAGGGGCTGAG  
CTGCCACCAGAGGTCTGGGACCCCTCACTTTAGTTCTTGGTATTTATTTTCTCCATCTCCACCTCCTTCATCC  
AGATAACTTATACATTCCCAAGAAAGTTCAGCCCAGATGGAAGGTGTTTCAAGGAAAGGTGGGCTGCCTTTTCCCC  
TTGTCTTATTTAGCGATGCCGCCGGGCATTTAACACCCACCTGGACTTCAGCAGAGTGGTCCGGGGCGAACCAG  
CCATGGGACGGTCACCCAGCAGTGCCGGGCTGGGCTCTGCGGTGCGGTCCACGGGAGAGCAGGCCTCCAGCTGGA  
AAGGCCAGGCTGGAGCTTGCTCTTCACTTTTGTGGCAGTTTTAGTTTTTGTTTTTTTTTTTTAAATCAAA  
AAACAATTTTTTTTAAAAAAAAGCTTTGAAAATGGATGTTTGGGTATTAAAAAGAAAAAAACTTAAAAAA  
AAAAGACACTAACGGCCAGTGAGTTGGAGTCTCAGGGCAGGGTGCCAGTTCCTTGAGCAAGCAGCCAGACGT  
TGAAGTGTGTTTCTTCCCTGGGCGCAGGGTGCCAGGTGCTTCCGGATCTGGTGTGACCTTGGTCCAGGAGTT  
CTATTTGTTCCTGGGAGGGAGGTTTTTTTTGTTGTTTTTGGGTTTTTTTGGTGTCTTGTCTTTCTCTCTCC  
ATGTGTCTTGGCAGGCACTCATTTCTGTGGCTGTGCGCCAGAGGGAATGTTCTGGAGCTGCCAAGGAGGGAGGAG  
ACTCGGGTTGGCTAATCCCCGGATGAACGGTGCTCCATTGCGACCTCCCTCCTCGTGCCTGCCCTGCCTCTCCA  
CGCACAGTGTAAAGGAGCCAAGAGGAGCCACTTCGCCAGACTTTGTTTCCCCACCTCCTGCGGCATGGGTGTGT  
CCAGTGCCACCGCTGGCCTCCGCTGCTTCCATCAGCCCTGTGCGCACCTGGTCTTCAATGAAGAGCAGACACTTA  
GAGGCTGGTGGGAATGGGGAGGTGCGCCCTGGGAGGGCAGGCGTTGGTTCCAAGCCGTTCCCGTCCCTGGCGC  
CTGGAGTGACACAGCCAGTCGGCACCTGGTGGCTGGAAGCCAACCTGCTTTAGATCACTCGGGTCCCCACCTT  
AGAAGGGTCCCCGCTTAGATCAATCACGTGGACACTAAGGCACGTTTTAGAGTCTCTTGTCTTAATGATTATGT  
CCATCCGTCTGTCCGTCCATTTGTGTTTTCTGCGTCTGTCATTGGATATAATCCTCAGAAATAATGCACACTAG  
CCTCTGACAACCATGAAGCAAAAATCCGTTACATGTGGTCTGAACTTGTAAGTCTCGGTACAGTATCAATAAA  
ATCTATAACAGAAAAA

416/615

**FIGURE 412**

MRQTIKVIKFIILICYTVYYVHNIKFDVDCTVDIESLTGYRTYRCAHPLATLFKILASFYIS  
LVIFYGLICMYTLWWMLRRSLKKYSFESIREESSYSDIPDVKNDFAFMLHLIDQYDPLYSKRF  
AVFLSEVSENKLRQLNLNNEWTLDKLRQRLTKNAQDKLELHLFMLS GIPDTVFDLVELEVLKL  
ELIPDVTIPPSIAQLTGLKELWLYHTAAKIEAPALAFLENLRALHIKFTDIKEIPLWIYSLK  
TLEELHLTGNLSAENNRYIVIDGLRELKRLKVLRLKSNLSKLPQVVTDVGVHLQKLSINNEG  
KLIVLNSLKKMANLTELELIRCDLERIPHSIFSLHNLQEIDLKDNNLKTIEEIIISFQHLHRLT  
CLKLWYNHIAIYIPIQIGNLTNLERLYLNRNKIEKIPTQLFYCRKLRYDLSHNNLTFLPADIG  
LLQNLQNLAITANRIETLPPPELFQCRKLRLHLGNNVLQSLPSRVGELTNLTQIELRGNRLEC  
LPVELGECPLLKRSGLVVEEDLFNTLPPEVKERLWRADKEQA

**Transmembrane domain:**

amino acids 51-75 (type II)

**N-glycosylation site.**

amino acids 262-266, 290-294, 328-332, 396-400, 432-436, 491-495

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 85-89

**Casein kinase II phosphorylation site.**amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368,  
398-402, 493-497**N-myristoylation site.**

amino acids 173-179, 261-267, 395-401, 441-447

417/615

**FIGURE 413**

GAATCATCCACGCACCTGCAGCTCTGCTGAGAGAGTGAAGCCGTGGGGGTTTTGAGCTCATC  
TTCATCATTTCATATGAGGAAATAAGTGGTAAAATCCTTGGAATACAAATGAGACTCATCAGAA  
ACATTTACATATTTTGTAGTATTGTTATGACAGCAGAGGGTGATGCTCCAGAGCTGCCAGAAG  
AAAGGGAACTGATGACCAACTGCTCCAACATGTCTTAAGAAAGGTTCCCGCAGACTTGACCC  
CAGCCACAACGACACTGGATTTATCCTATAACCTCCTTTTTCAACTCCAGAGTTCAGATTTTC  
ATTCTGTCTCCAAACTGAGAGTTTTGATTCTATGCCATAACAGAATTCACAGCTGGATCTCA  
AAACCTTTGAATTCAACAAGGAGTTAAGATATTTAGATTTGTCTAATAACAGACTGAAGAGTG  
TAACCTGGTATTTACTGGCAGGTCTCAGGTATTTAGATCTTTCTTTAATGACTTTGACACCA  
TGCCTATCTGTGAGGAAGCTGGCAACATGTCACACCTGGAATCCTAGGTTTGAGTGGGGCAA  
AAATACAAAAATCAGATTTCCAGAAAATGCTCATCTGCATCTAAATACTGTCTCTTAGGAT  
TCAGAACTCTTCCTCATTATGAAGAAGGTGACCTGCCCATCTTAAACACAACAAAACCTGCACA  
TTGTTTTACCAATGGACACAAATTTCTGGGTCTTTTGCCTGATGGAATCAAGACTTCAAAAA  
TATTAGAAATGACAAATATAGATGGCAAAAGCCAATTTGTAAGTTATGAAATGCAACGAAATC  
TTAGTTTAGAAAAATGCTAAGACATCGGTTCTATTGCTTAATAAAGTTGATTTACTCTGGGACG  
ACCTTTTCTTATCTTACAATTTGTTTGGCATAACATCAGTGGAACTTTTCAATCTGAAATG  
TGACTTTTGGTGGTAAGGCTTATCTTGACCAATTCATTTGACTACTCAAATACTGTAATGA  
GAATATAAAATTTGGAGCATGTACATTTTCAAGAGTGTGTTTACATTCAACAGGATAAAATCTATT  
TGCTTTTGGACAAAATGGACATAGAAAACCTGACAATATCAATGCACAAATGCCACACATGC  
TTTTCCCGAATTATCCTACGAAATTCCAATATTTAAATTTTGCCAATAATATCTTAACAGACG  
AGTTGTTTTAAAAGAACTATCCAACCTGACCTGCAATTTGAAAACCTCTCATTTTGAATGGCAATAAC  
TGGAGACACTTTCTTTAGTAAGTTGCTTTGCTAACACACACACCCTTGGAACACTTGGATCTGA  
GTCAAAATCTATTACAACATAAAATGATGAAAATTGCTCATGGCCAGAACTGTGGTCAATA  
TGAATCTGTATACATAAAATTTGCTGATTCTGTCTTCAGGTGCTTGCCCAAAGTATTCAA  
TACTTGACCTAAATAATAACCAATCCAACTGTACCTAAAGAGACTATTCATCTGATGGCCT  
TACGAGAACTAAATATTGCATTTAATTTTCTAACTGATCTCCCTGGATGCAGTCATTTAGTA  
GACTTTTCACTTCTGAACATTGAAATGAACCTTCTCTCAGCCCATCTCTGGATTTTGTTCAGA  
GCTGCCAGGAAGTTAAACTCTAAATGCGGGAAGAAATCCATTCCGGTGTACCTGTGAATTAA  
AAAATTTTCACTCAGCTTGAAACATATTGAGAGGTGATGATGGTTGGATGGTCAAGATTCATACA  
CCTGTGAATACCCCTTTAAACCTAAGGGGAAGTAAAGACGTTTCTCTCCACGAATTTAT  
CTTGCAACACAGCTCTGTTGATTGTCAACATTTGCTGTTGTTTATTGCTAGTTCTGGGGTTGGCTG  
TGGCCTTCTGCTGTCTCCACTTTGATCTGCCCTGGTATCTCAGGATGCTAGGTCAATGCACAC  
AAACATGGCACAGGGTTAGGAAAACAACCCAAGAACAACTCAAGAGAAATGTCCGATTCCACG  
CATTTATTTTATACAGTGAACATGATTCTCTGTGGGTGAAGAATGAATTGATCCCCAATCTAG  
AGAAGGAAGATGGTTCTATCTTGATTTGCTTTTATGAAAGCTACTTTGACCTGGCAAAAGCA  
TTAGTGAAAATATTGTAAGCTTCAATTGAGAAAAGCTATAAGTCCATCTTTGTTTTGTCTCCCA  
ACTTTGTCCAGAATGAGTGGTGCCATTATGAATTTCTACTTTGCCCAACCAATCTCTTCCATG  
AAAATTTCTGATCATATAATTCTTATCTTACTGGAACCCATTCCATTCTATTGCATTCCACCA  
GGTATCATAAACTGAAAGCTCTCCTGGAAAAAAAGCATACTTGGAATGGCCCAAGGATAGGC  
GTAAATGTGGGCTTTTCTGGGCAACCTTCGAGCTGCTATTAAATGTTAATGTATTAGCCACCA  
GAGAAATGTATGAACTGCAGACATTCACAGAGTTAAATGAAGAGTCTCGAGGTTCTACAATCT  
CTCTGATGAGAACAGATTGTCTATAAAATCCACAGTCCTTGGAAGTTGGGGACCACATACA  
CTGTTGGGATGTACATTGATACAACTTTATGATGGCAATTTGACAATATTTATTAAAAATAAA  
AAATGGTTATTTCCCTTCATATCAGTTTCTAGAAGGATTTCTAAGAATGTATCCTATAGAAACA  
CCTTCACAAGTTTATAAGGGCTTATGGAAGGTTGTTTCATCCCAGGATTTTATAATCATG  
AAAAATGTGGCCAGGTGCAGTGGCTCACTCTTGAATCCCAGCACTATGGGAGGCCAAGGTGG  
GTGACCCACGAGGTCAAGAGATGGAGACCATCCTGGCCAACATGGTGAAACCTGTCTCTACT  
AAAAATACAAAATTAGCTGGGCGTGATGGTGCACGCCTGTAGTCCCAGCTACTTTGGGAGGCT  
GAGGCAGGAGAATCGCTTGAACCCGGGAGGTGGCAGTTGCAGTGAGCTGAGATCGAGCCACTG  
CACTCCAGCCTGGTGACAGAGCGAGACTCCATCTCAAAAAAAGAAAAAAGAAAAA  
ATGGAACATCCTCATGGCCACAAAATAAGGTCTAATTCAATAAATTATAGTACATTAATGT  
AATATAATATTACATGCCACTAAAAAGAATAAGGTAGCTGTATATTTCTGGTATGGAAAAA  
CATATTAATATTGTTATAAACTATTAGTTGGTGCAAACTAATTGTGGTTTTTGGCATTGAAA  
TGGCATTGAAATAAAGTGTAAAGAAATCTATACAGATGTAGTAACAGTGTTTGGGTCTGG  
GAGGTTGGATTACAGGGAGCATTTGATTTCTATGTTGTGATTTCTATAATGTTGATTTGTT  
TAGAATGAATCTGTATTTCTTTTATAAGTAGAAAAAATAAAGATAGTTTTTACAGCCT



418/615

**FIGURE 414**

MRLIRNIYIFCSIVMTAEGDAPELPEERELMTNCSNMSLRKVPADLTPATTTLDLSYNLLFQL  
QSSDFHSVSKLRVLILCHNRIQQDLKTFFFNKELRYLDLSNNRLKSVTWYLLAGLRYLDLSF  
NDFDTMPICEEAGNMSHLEILGLSGAKIQKSDFQKIAHLHLNTVFLGFRTLPHYEEGSLPILN  
TTKLHIVLPMDTNFWVLLRDGIKTSKILEMTNIDGKSQFVSYEMQRNLSLENAKTSVLLLNKV  
DLLWDDLFLILQFVWHTSVEHFQIRNVTFGGKAYLDHNSFDYSNTVMRTIKLEHVHFRVFIQ  
QDKIYLLLTkMDIENLTISNAQMPHMLFPNYPTKFQYLNFAANNILTDELfKRTIQLPHLKTli  
LNGNKLETLSLVSCFANNTPLEHLDLSONLLQHKNDENCWPETVVNMNLSYNKLSDSVFRCL  
PKSIQILDNNNNQIQTVPKETIHLMALRELNIAFNFLTDLPGCshFSRLSVLNIEMNFILSPS  
LDFVQSCQEVKTLNAGRNPFRCTCELKNFIQLETYSEVMVGWSDSYTCEYPLNLRGTRLKDV  
HLHELSCNTALLIVTIVVIMLVGLAVAFCClHFDLPWYLRMLGQCTQTWHRVRKTTQEQLKR  
NVRFHAFISYSEHDSLWVKNELIPNLEKEDGSILICLYESYFDPGKSISENIVSFIEKSYKSI  
FVLSPNFVQNEWCHYEFYFAHNNLFHENSdHIILILLEPIPFYCIPTRYHKLKALLEKKAYLE  
WPKDRRKCGLFWANLRAAINVNVLATREMYELQTFTELNEESRGSTISLMRTDCL

419/615

**FIGURE 415**

CGGACGCGTGGGCGGACGCGTGGGCCTGGGCAAGGGCCGGGGCGCCGGGCGGAGCCACCTCTTCCCCTCCCCCGC  
TTCCCTGTGCGGCTCCGCTGGCTGGACGCGCTGGAGGAGTGGAGCAGCACCCGGCCGGCCCTGGGGGCTGACAGT  
CGGCAAAAGTTTGGCCCCGAAGAGGAAGTGGTCTCAAACCCCGGAGGTGGCGACAGGCCAGACCAGGGGCGCTCG  
CTGCCTGCGGGCGGGCTGTAGGCGAGGGCGCGCCCCAGTGCCGAGACCCGGGGCTTCAGGAGCCGGCCCCGGGAG  
AGAAGAGTGGGGCGGCGGACGGAGAAAACAACCTCAAAGTTGGCGAAAGGCACCGCCCTACTCCCGGGCTGCCG  
CCGCTCCCCGCCCCAGCCCTGGCATCCAGAGTACGGGTGAGCCCGGGCCATGGAGCCCCCTGGGGAGGCGG  
CACCAGGGAGCCTGGGCGCCCGGGGCTCCGCCGCGACCCCATCGGGTAGACCACAGAAGCTCCGGGACCCCTCCG  
GCACCTCTGGACAGCCAGGATGCTGTTGGCCACCTCCTCCTCCTCCTTGGAGGCGCTCTGGCCCATCCAG  
ACCGGATTATTTTCCAAATCATGCTTGTGAGGACCCCCAGCAGTGCTCTTAGAAGTGCAGGGCACCTTACAGA  
GGCCCTGGTCCGGGACAGCCGACCTCCCTGCCAACTGCACCTGGCTCATCCTGGGCAGCAAGGAACAGACTG  
TCACCATCAGGTTCCAGAAGCTACACCTGGCTGTGGCTCAGAGCGCTTAACCTACGCTCCCTCTCCAGCCAC  
TGATCTCCCTGTGTGAGGCACCTCCAGCCCTCTGCAGCTGCCCGGGGCAACGTACCATCACTTACAGCTATG  
CTGGGGCCAGAGCACCCATGGGCCAGGGCTTCCTGCTCTCCTACAGCCAAGATTGGCTGATGTGCTGCAGGAAG  
AGTTTCAGTGCTGAACACCGCTGTGTATCTGCTGTCCAGCGCTGTGATGGGGTTGATGCCTGTGGCGATGGCT  
CTGATGAAGCAGGTTGCAGCTCAGACCCCTTCCCTGGCCTGACCCCAAGACCCGTCCCTCCCTGCCTTGCAATG  
TCACCTTGGAGGACTTCTATGGGGTCTTCTCCTCCTGGATATACACCTAGCCTCAGTCTCCCAACCCAGT  
CCTGCCATTGGCTGCTGGACCCCATGATGGCCGGCGGCTGGCCGTGCGCTTCACAGCCCTGGACTTGGGCTTTG  
GAGATGCAGTGCATGTGTATGACGGCCCTGGGCCCTGAGAGCTCCCGACTACTGCGTAGTCTACCCACTTCA  
GCAATGGCAAGGCTGTCACTGTGGAGACACTGTCTGGCCAGGCTGTTGTGTCTACCACACAGTTGCTTGGAGCA  
ATGGTCGTGGCTTCAATGCCACCTACCATGTGCGGGGCTATTGCTTGCCTTGGGACAGACCCTGTGGCTTAGGCT  
CTGGCCTGGGAGCTGGCGAAGGCCTAGGTGAGCGCTGTACAGTGAGGCACAGCGCTGTGACGGCTCATGGGACT  
GTGCTGACGGCAGATGAGGAGGACTGCCAGGCTGCCACCTGGACACTTCCCTGTGGGGCTGCTGGCACCT  
CTGGTGCCACAGCCTGTACCTGCCTGCTGACCGCTGCAACTACCAGACTTCTGTGCTGATGGAGCAGATGAGA  
GACGCTGTGCGCATTTGCCAGCCTGGCAATTTCCGATGCCGGGACGAGAAGTGCGTGTATGAGACGTGGGTGTGCG  
ATGGGCAGCCAGACTGTGCGGACGGCAGTGATGAGTGGGACTGCTCCTATGTTCTGCCCCGCAAGGTCAATACAG  
CTGCAGTCATTGGCAGCCTAGTGTGCGGCCTGCTCCTGGTCATCGCCCTGGGCTGCACCTGCAAGCTCTATGCCA  
TTGCAACCCAGGAGTACAGCATCTTTGCCCCCTCTCCCGATGGAGGCTGAGATTGTGCAGCAGCAGGCACCCC  
CTTCTACGGGCAGCTCATTGCCAGGGTGCCATCCCACCTGTAGAAGACTTTCCTACAGAGAATCCTAATGATA  
ACTCAGTGCTGGGCAACCTGCGTTCTCTGCTACAGATCTTACGCCAGGATATGACTCCAGGAGGTGGCCAGGTG  
CCCGCCGTCGTACGCGGGGCGCTTGATGCGACGCTGGTACGCCGTCTCCGCCGCTGGGGCTTGCTCCCTCGAA  
CCAACACCCCGGCTCGGGCCTCTGAGGCCAGATCCAGGTCAACCTTCTGCTGCTCCCTTGAGGCCCTAGATG  
GTGGCAGAGTCCAGCCCGTGAGGGCGGGGAGTGGGTGGGCAAGATGGGGAGCAGGCACCCCCACTGCCCATCA  
AGGCTCCCTCCCATCTGCTAGCACGTCTCAGCCCCACTACTGTCCCTGAAGCCCAGGGCCACTGCCCTCAC  
TGCCCCTAGAGCCATCACTATTGTCTGGAGTGGTGACGGCCCTGCGAGGCCGCTGTTGCCAGCCTGGGGCCCC  
CAGGACCAACCCGGAGCCCCCTGGACCCACACAGCAGTCTGGCCCTGGAAGATGAGGACGATGTGCTACTGG  
TGCCACTGGCTGAGCCGGGGGTGTGGGTAGCTGAGGCAGAGGATGAGCCACTGCTTACCTGAGGGGACCTGGGGG  
CTCTACTGAGGCCTCTCCCTGGGGGCTTACTCATAGTGGCACAACTTTTAGAGGTGGGTGACCTCCCTCC  
ACCACTTCCTTCCCTGTCCCTGGATTTAGGGACTTGGTGGGCCTCCCGTTGACCTATGTAGCTGTATATAAGT  
TAAGTGTCCCTCAGGCAGGGAGAGGGCTCACAGAGTCTCCTGTACGTGGCCATGGCCAGACCCCACTCCCT  
TCACCACCACTGCTCCCCACGCCACCACCTTTGGGTGGCTGTTTTTAAAAAGTAAAGTTCTTAGAGGATCATA  
GGTCTGGACACTCCATCCTTGCCAAACCTCTACCCAAAAGTGGCCTTAAGCACCGGAATGCCAATTAAGTAGAGA  
CCCTCCAGCCCCAAGGGGAGGATTTGGGCAGAACCTGAGGTTTTGCCATCCACAATCCCTCCTACAGGGCCTGG  
CTCACAAAAGAGTGCAACAAATGCTTCTATTCCATAGCTACGGCATTGCTCAGTAAGTTGAGGTCAAAAATAAA  
GGAATCATACATCTC

420/615

**FIGURE 416**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49631  
<subunit 1 of 1, 713 aa, 1 stop  
<MW: 76193, pI: 5.42, NX(S/T): 4  
MLLATLLLLLLGGALAHDPRIIFPNHACEDPPAVLLEVQGTLQRPFLVRDSRTSPANCTWLILG  
SKEQTVTIRFQKLHLACGSERLTLRSPLQPLISLCEAPPSPLQLPGGNVTITYSYAGARAPMG  
QGFLLSYSQDWLMCLQEEFQCLNHRCVSAVQRCGDGVDACGDGSDEAGCSSDPFFGLTPRPVPS  
LPCNVTLEDFYGVFSSPGYTHLASVSHPQSCHWLLDPHDGRRRLAVRFTALDLGFGDAVHVYDG  
PGPPESSRLLRSLTHFSNGKAVTVETLSGQAVVSYHTVAWSNGRGFNATYHVRGYCLPWDRPC  
GLGSGLGAGEGLGERCYSEAQRCDGSWDCADGTDEEDCPGCPPGHFPCGAAGTSGATACYLPA  
DRCNYQTFCADGADERRCRHCQPGNFRCDKCVYETWVCDGQPDGQDCADGSDEWDCSYVLPRKV  
ITAAVIGSLVCGLLLVIALGCTCKLYAIRTQEYSIFAPLSRMEAEIVQQQAPPSYQQLIAQGA  
IPPVEDFPTENPNDNSVLGNLRSLLQILRQDMTPGGGPGARRRQRGRIMRRLVRRLLRWGLLP  
RTNTPARASEARSQVTPSAAPLEALDGGTGPAREGGAVGGQDGEQAPPLPIKAPLPSASTSPA  
PTTVPEAPGPLPSLPLEPSLLSGVVQALRGRLPSLGPPEGPTRSPPGPHTAVLALEDEDDVLL  
VPLAEPGVWVAEAEDEPLLT

**Important features:****Signal peptide:**

amino acids 1-16

**Transmembrane domain:**

amino acids 442-462

**LDL-receptor class A (LDLRA) domain proteins**

amino acids 411-431, 152-171, 331-350 and 374-393

421/615

**FIGURE 417**

GTCGTTCCCTTTGCTCTCTCGCGCCAGTCCTCCTCCCTGGTTCTCCTCAGCCGCTGTGCGAGGAGAGCACC CGGA  
GACGCGGGCTGCAGTCGCGGCGGCTTCTCCCCGCTGGGCGGCTCGCCGCTGGGCAGGTGCTGAGCGCCCTAG  
AGCCTCCCTTGCCGCTCCCTCCTCTGCCCCGCCGAGCAGTGCACATGGGGTGTGGAGGTAGATGGGCTCCCG  
GCCCCGGAGGCGCGGTGGATGCGGCGCTGGGCAGAAAGCAGCCGCCGATTCCAGCTGCCCGCGCGCCCCGGGCG  
CCCCTGCGAGTCCCCGGTT CAGCCATGGGGACCTCTCCGAGCAGCAGCACCGCCCTCGCCTCCTGCAGCCGCATC  
GCCCGCCGAGCCACAGCCACGATGATCGGGGCTCCCTTCTCCTGCTTGGATTCTTAGCACCACCACAGCTCAG  
CCAGAACAGAAGGCCTCGAATCTCATTGGCACATACCGCCATGTTGACCGTGCCACCGGCCAGGTGCTAACCTGT  
GACAAGTGTCCAGCAGGAACCTATGTCTCTGAGCATTGTACCAACACAAGCCTGCGCGTCTGCAGCAGTTGCCCT  
GTGGGGACCTTTACCAGGCATGAGAATGGCATAGAGAAATGCCATGACTGTAGTCAGCCATGCCCATGGCCAATG  
ATTGAGAAATTACCTTGTGCTGCCTTGACTGACCGAGAATGCACTTGCCACCTGGCATGTTCCAGTCTAACGCT  
ACCTGTGCCCCCATAACGGTGTGCTGTGGGTGGGGTGTGCGGAAGAAAGGGACAGAGACTGAGGATGTGCGG  
TGTAAGCAGTGTGCTCGGGGTACCTTCTCAGATGTGCTTCTAGTGTGATGAAATGCAAAGCATAACAGACTGT  
CTGAGTCAGAACCTGGTGGTGATCAAGCGGGGACCAAGGAGACAGACAACGCTCTGTGGCACACTCCCGTCTTTC  
TCCAGCTCCACCTCACCTTCCCCTGGCACAGCCATCTTTCCACGCCCTGAGCACATGGAACCCATGAAGTCCCT  
TCCTCCACTTATGTTCCCAAAGGCATGAACCTCAACAGAATCCAACCTCTTCTGCCTCTGTTAGACCAAAGGTACTG  
AGTAGCATCCAGGAAGGGACAGTCCCTGACAACACAAGCTCAGCAAGGGGGAAGGAAGACGTGAACAAGACCCTC  
CCAAACCTTCAGTAGTCAACCACCAGCAAGGCCCCACCACAGACACATCCTGAAGCTGCTGCCGTCCATGGAG  
GCCACTGGGGGCGAGAAGTCCAGCACGCCCATCAAGGGCCCCAAGAGGGGACATCCTAGACAGAACCTACACAAG  
CATTTTGACATCAATGAGCATTTGCCCTGGATGATTGTGCTTTTCTGCTGCTGGTGCTTGTGGTGATTGTGGTG  
TGCAATATCCGGAAGCTCGAGGACTCTGAAAAGGGGCCCCGGCAGGATCCAGTGCCATTGTGAAAAGGCA  
GGGCTGAAGAAATCCATGACTCCAACCCAGAACCGGGGAGAAATGGATCTACTACTGCAATGGCCATGGTATCGAT  
ATCCTGAAGCTTGTAGCAGCCCAAGTGGGAAGCCAGTGGAAAGATATCTATCAGTTTCTTTGCAATGCCAGTGAG  
AGGGAGGTGTGCTGCTTCTCCAATGGGTACACAGCCGACCAGCAGCGGGCTACGCAGCTCTGCAGCACTGGACC  
ATCCGGGGCCCCGAGGCCAGCCTCGCCAGCTAATTAGCGCCCTGCGCCAGCACCGGAGAAACGATGTTGTGGAG  
AAGATTGCTGGGCTGATGGAAGACACCACCCAGCTGGAAACTGACAACTAGCTCTCCCGATGAGCCCCAGCCCCG  
CTTAGCCCCGAGCCCCATCCCCAGCCCCAACGCCAACTTGAGAATTCGGCTCTCCTGACGGTGGAGCCTTCCCCA  
CAGGACAAGAACAAGGGCTTCTTCGTGGATGAGTCGGAGCCCCCTTCTCCGCTGTGACTCTACATCCAGCGGCTCC  
TCCGCGCTGAGCAGGAACGGTTCCTTTATTACCAAGAAAAGAAGGACACAGTGTGCGGCAGGTACGCCTGGAC  
CCCTGTGACTTGCAGCCTATCTTTGATGACATGCTCCACTTTCTAAATCCTGAGGAGCTGCGGGTGATTGAAGAG  
ATTCCCCAGGCTGAGGACAACTAGACCGGCTATTTCGAAATTATTGGAGTCAAGAGCCAGGAAGCCAGCCAGACC  
CTCCTGGACTCTGTTTATAGCCATCTTCTGACCTGCTGTAGAACATAGGGATACTGCATTCTGGAAATTACTCA  
ATTTAGTGGCAGGGTGGTTTTTTAATTTTCTTCTGTTTCTGATTTTTGTTGTTTGGGGTGTGTGTGTGTGTTTGT  
GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTTTAAACAGAGAATATGGCCAGTGCTTGAGTCTTTTCTCCTTCTC  
TCTCTCTTTTTTTTTTTAAATAACTCTTCTGGGAAGTTGGTTTTATAAGCCTTTGCCAGGTGTAAGTGTGTGAA  
ATACCCACCACTAAAGTTTTTTAAGTTCATATTTTCTCCATTTTGCCCTTCTTATGTATTTTCAAGATTATTCTG  
TGCATTTTAAATTTACTTAACTTACCATAAATGCAGTGTGACTTTTCCACACACTGGATTGTGAGGCTCTTAAC  
TTCTTAAAGTATAATGGCATCTTGTGAATCCTATAAGCAGTCTTTATGTCTCTTAACATTACACCTACTTTTT  
AAAAACAAATATTATTACTATTTTATTATTGTTTGTCTTTATAAATTTTCTTAAAGATTAAAGAAATTTAAGA  
CCCCATTGAGTTACTGTAATGCAATTCACTTTGAGTTATCTTTAAATATGTCTTGTATAGTTTCAATTCATGG  
CTGAAACTTGACCACACTATTGCTGATTGTATGTTTTACCTGGACACCGTGTAAGTGTGTTGATTACTTGTAC  
TCTTCTTATGCTAATATGCTCTGGGCTGGAGAAATGAAATCCTCAAGCCATCAGGATTTGCTATTTAAGTGGCTT  
GACAAGTGGGCCACCAAGAACTTGAACCTTACCTTTTAGGATTTGAGCTGTTCTGGAACACATTGCTGCACTTT  
GGAAAGTCAAAATCAAGTGCCAGTGGCGCCCTTTCCATAGAGAATTTGCCAGCTTTGCTTTAAAGATGTCTTG  
TTTTTTATATACACATAATCAATAGGTCCAATCTGCTCTCAAGGCCTTGGTCCTGGTGGGATTCTTCCACCAATT  
ACTTTAATTTAAATGGCTGCAACTGTAAGAACCCTTGTCTGATATATTTGCAACTATGCTCCCATTTACAAATG  
TACCTTCTAATGCTCAGTTGCCAGGTTCCAATGCAAAGGTGGCGTGGACTCCCTTTGTGTGGGTGGGGTTTGTGG  
GTAGTGGTGAAGGACCGATATCAGAAAAATGCCTTCAAGTGTACTAATTTATTAATAACATTAGGTGTTTGTTA  
AAAAAAA

422/615

**FIGURE 418**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52594  
><subunit 1 of 1, 655 aa, 1 stop  
><MW: 71845, pI: 8.22, NX(S/T): 8  
MGTSPPSSSTALASCSRIARRATATMIAGSLLLLGFLSTTTAQPEQKASNLIGTYRHVDRATGQ  
VLTCDKCPAGTYVSEHCTNTSLRVCSSCPVGTFTRHENGIEKCHDCSQPCPWPMIEKLPCAAL  
TDRECTCPPGMFQSNATCAPHTVCPVGWGVRRKGTETEDVRCKQCARGTFSDVPSSVMKCKAY  
TDCLSQNLVVIKPGTKETDNVCGTLPFSSTSPSPGTAFPRPEHMETHEVPSSTYVPGGMN  
STESNSSASVRPKVLSSIQEGTVPDNTSSARGKEDVNKTLPNLQVNVHQGPVHRHILKLLPS  
MEATGGEKSSTPIKGPKRGHPRQNLHKHFDINEHLPWMIVLFLLLVLVVIIVVCSIRKSSRTLK  
KGPRQDPSAIVEKAGLKKSMTPTQNREKWIYYCNGHGIDILKLVAQVGSQWKDIYQFLCNAS  
EREVAAFNGYTADHERAYAALQHWITIRGPEASLAQLISALRQHRNDVVEKIRGLMEDTTQL  
ETDKLALPMSPLSPSPIPSPNAKLENSALLTVEPSPQDKNKGFFVDESEPLLRCSTSSGS  
SALSRNGSFITKEKKDVTVLQVRLDPCDLQPIFDDMLHFLNPEELRVIEEIPQAEDKLDRLFE  
IIGVKSQEASQTL LDSVYSHLPDLL

**Signal sequence:**

amino acids 1-41

**Transmembrane domain:**

amino acids 350-370

423/615

**FIGURE 419**

ATGGCTGGTGACGGCGGGGCCGGGCAGGGGACCGGGGCCGGCCGGGAGCGGGCCAGCTGCCGGGAGCCCTGA  
ATCACCGCCTGGCCCGACTCCACCATGAACGTCGCGCTGCAGGAGCTGGGAGCTGGCAGCAACGTGGGATTCCAG  
AAGGGGACAAGACAGCTGTTAGGCTCACGCACGCAGCTGGAGCTGGTCTTAGCAGGTGCCTCTCTACTGCTGGCT  
GCACTGCTTCTGGGCTGCCTTGTGGCCCTAGGGGTCCAGTACCACAGAGACCCATCCCACAGCACCTGCCTTACA  
GAGGCCTGCATTGAGTGGCTGGAAAAATCCTGGAGTCCCTGGACCGAGGGGTGAGCCCCTGTGAGGACTTTTAC  
CAGTTCTCCTGTGGGGGCTGGATTTCGGAGGAACCCCTGCCGATGGGCGTTCTCGCTGGAACACCTTCAACAGC  
CTCTGGGACAAAACCAGGCCATACTGAAGCACCTGCTTGAAAACACCACCTTCAACTCCAGCAGTGAAGCTGAG  
CAGAAGACACAGCGCTTCTACCTATCTTGCCTACAGGTGGAGCGCATTGAGGAGCTGGGAGCCCAGCCACTGAGA  
GACCTCATTGAGAAGATTGGTGGTTGGAACATTACGGGGCCCTGGGACCAGGACAACCTTTATGGAGGTGTTGAAG  
GCAGTAGCAGGGACCTACAGGGCCACCCCATTTCTCACCGTCTACATCAGTGCCGACTCTAAGAGTTCCAACAGC  
AATGTTATCCAGGTGGACAGTCTGGGCTCTTCTGCCCTCTCGGGATTACTACTTAAACAGAACTGCCAATGAG  
AAAGTGCTCACTGCCCTATCTGGATTACATGGAGGAACCTGGGGATGCTGCTGGGTGGGCGGCCACCTCCACGAGG  
GAGCAGATGCAGCAGGTGCTGGAGTTGGAGATACAGCTGGCCAACATCACAGTGCCCCAGGACCAGCGCGCGAC  
GAGGAGAAGATCTACCACAAGATGAGCATTTCGGAGCTGCAGGCTCTGGCGCCCTCCATGGACTGGCTTGAGTTC  
CTGTCTTCTTGTGTGTCACCATTTGGAGTTGAGTACTCTGAGCCTGTGGTGGTGTATGGGATGGATTATTTGCAG  
CAGGTGTCAGAGCTCATCAACGCACGGAACCAAGCATCCTGAACAATTACCTGATCTGGAACCTGGTGCAAAAG  
ACAACCTCAAGCCTGGACCGACGCTTTGAGTCTGCACAAGAGAAGCTGCTGGAGACCCCTATGGCACTAAGAAG  
TCCTGTGTGCCGAGGTGGCAGACCTGCATCTCCAACACGGATGACGCCCTTGGCTTTGCTTTGGGGTCACTCTTC  
GTGAAGGCCACGTTTGACCGGCAAAGCAAAGAAATTGCAGAGGGGATGATCAGCGAAATCCGGACCGCATTGAG  
GAGGCCCTGGGACAGCTGGTTTGGATGGATGAGAAGACCGCCAGGCAGCCAAGGAGAAAGCAGATGCCATCTAT  
GATATGATTGGTTTCCCAGACTTTATCCTGGAGCCCCAAAGAGCTGGATGATGTTTATGACGGGTACGAAATTTCT  
GAAGATTCTTCTTCCAAAACATGTTGAATTTGTACAACCTTCTTGCCAAGGTTATGGCTGACCAGCTCCGCAAG  
CCTCCCAGCCGAGACCACTGGAGCATGACCCCCAGACAGTGAATGCCTACTACCTTCCAACCTAAGAATGAGATC  
GTCTTCCCCGCTGGCATCCTGCAGGCCCCCTTCTATGCCCGCAACCAACCCCAAGGCCCTGAACTTCGGTGGCATC  
GGTGTGGTGCATGGGCCATGAGTTGACGCATGCCTTTGATGACCAAGGGCGCGAGTATGACAAAGAAGGGAACCTG  
CGGCCCTGGTGGCAGAATGAGTCCCTGGCAGCCTTCCGGAACACACGGCCTGCATGGAGGAACAGTACAATCAA  
TACCAGGTCAATGGGGAGAGGCTCAACGGCCGCCAGACGCTGGGGGAGAACATTACTGACAACGGGGGGGCTGAAG  
GCTGCCTACAATGCTTACAAAGCATGGCTGAGAAAGCATGGGGAGGAGCAGCAACTGCCAGCCGTGGGGCTCACC  
AACCACCAGCTCTTCTTCGTGGGATTTGCCAGGTGTGGTGTCTGGTCCGTCACACCAGAGAGCTCTCACGAGGGG  
CTGGTGACCGACCCCCACAGCCCTGCCCGCTTCCGCGTGTGGGCACTCTCTCCAACCTCCCGTGACTTCTGCGG  
CACTTCGGCTGCCCTGTTCGGCTCCCCCATGAACCCAGGGCAGCTGTGTGAGGTGTGGTAGACCTGGATCAGGGGA  
GAAATGGCCAGCTGTCAACAGACCTGGGGCAGCTCTCCTGACAAAGCTGTTTGCTCTTGGGTTGGGAGGAAGCAA  
ATGCAAGCTGGGCTGGGTCTAGTCCCTCCCCCCACAGGTGACATGAGTACAGACCCCTCCTCAATCACCACATTG  
TGCTCTGCTTTGGGGGTGCCCTGCCCTCCAGCAGAGCCCCCACCATTCACTGTGACATCTTCCGTGTACCCT  
GCCTGGAAGAGGTCTGGGTGGGAGGCCAGTTCCCATAGGAAGGAGTCTGCC

424/615

**FIGURE 420**

MNVALQELGAGSNVGFQKGTRQLLGSRTQLELVLAGASLLLAALLLGCLVALGVQYHRDPSHS  
TCLTEACIRVAGKILES LDRGVSPCEDFYQFSCGGWIRRNPLPDGRSRWNTFNSLWDQNQAIL  
KHLLENTTFNSSSEAEQKTQRFYLSCLQVERIEELGAQPLRD LIEKIGGWNITGPWDQDNFME  
VLKAVAGTYRATPFFTVYISADSKSSNSNVIQVDQSG LFLPSRDY YLNRTANEKVL TAYLDYM  
EELGMLLGGRPTSTREQMQQVLELEIQ LANITVPQDQRRDEEKIYHKMSISELQALAPSMDWL  
EFLSFLLSPLELSDSEPVVVYGMDYLQQVSELINRTEPSILNNYLIWNLVQKTSSSLDRRFES  
AQEK LLETLYGTTKSCVPRWQTCISNTDDALGFALGSLFVKATFDRQSKEIAEGMISEIRTA F  
EEALGQLVWMDEKTRQAAKEKADAIYDMIGFPDFILEPKELDDVYDGYEISEDSFFQNMLNLY  
NFSAKVMADQLRKPPSRDQWSMTPQTVNAYYLPTKNEIVFPAGILQAPFYARNHPKALNFGGI  
GVVMGHELTHAFDDQGREYDKEGNLRPWWQNESLA AFRNHTACMEEQYNQYQVNGERLNGRQT  
LGENITDNGGLKAAYNAYKAWLRKHGEEQQLPAVGLTNHQLFFVGFAQVWCSVRTPESSHEGL  
VTDPHSPARFRVLGTLSNSRDFLRHFGCPVGS PMNPGQLCEVW

**Type II Transmembrane domain:**  
amino acids 32-57

425/615

**FIGURE 421**

GGCGCCGCGTAGGCCCGGGAGGCCGGGCGGGCTGCGAGCGCCTGCCCATGCGCCGCC  
GCCTCTCCGCACG**ATG**TTCCCCCTCGCGGAGGAAAGCGGCGCAGCTGCCCTGGGAGGACGGCAG  
GTCCGGGTGCTCTCCGGCGGCCCTCCCTCGGAAGTGTTCCGTCTTCCACCTGTTTCGTGGCCTG  
CCTCTCGCTGGGCTTCTTCTCCCTACTCTGGCTGCAGCTCAGCTGCTCTGGGGACGTGGCCCG  
GGCAGTCAGGGGACAAGGGCAGGAGACCTCGGGCCCTCCCCGTGCCTGCCCCCAGAGCCGCC  
CCCTGAGCACTGGGAAGAAGACGCATCCTGGGGCCCCCACC GCCTGGCAGTGCTGGTGCCCTT  
CCGCGAACGCTTCGAGGAGCTCCTGGTCTTCGTGCCCCACATGCGCCGCTTCCTGAGCAGGAA  
GAAGATCCGGCACCACTCTACGTGCTCAACCAGGTGGACCACTTCAGGTTCAACCGGGCAGC  
GCTCATCAACGTGGGCTTCCTGGAGAGCAGCAACAGCACGGACTACATTGCCATGCACGACGT  
TGACCTGCTCCCTCTCAACGAGGAGCTGGACTATGGCTTTCCTGAGGCTGGGCCCTTCCACGT  
GGCCTCCCCGGAGCTCCACCCTCTCTACCACTACAAGACCTATGTCGGCGGCATCCTGCTGCT  
CTCCAAGCAGCACTACCGGCTGTGCAATGGGATGTCCAACCGCTTCTGGGGCTGGGGCCGCGA  
GGACGACGAGTTCTACCGGCGCATTAAGGGAGCTGGGCTCCAGCTTTTCCGCCCCCTCGGGAAT  
CACAAC TGGGTACAAGACATTTGCCCACCTGCATGACCCAGCCTGGCGGAAGAGGGACCAGAA  
GCGCATCGCAGCTCAAAAACAGGAGCAGTTCAAGGTGGACAGGGAGGGAGGCCTGAACACTGT  
GAAGTACCATGTGGCTTCCCGCACTGCCCTGTCTGTGGGCGGGGCCCCCTGCACTGTCCTCAA  
CATCATGTTGGACTGTGACAAGACCGCCACACCCTGGTGCACATTCAGCT**TCAG**CTGGATGGAC  
AGTGAGGAAGCCTGTACCTACAGGCCATATTGCTCAGGCTCAGGACAAGGCCTCAGGTTCGTGG  
GCCAGCTCTGACAGGATGTGGAGTGGCCAGGACCAAGACAGCAAGCTACGCAATTGCAGCCA  
CCCGGCCGCCAAGGCAGGCTTGGGCTGGGCCAGGACACGTGGGGTGCCTGGGACGCTGCTTGC  
CATGCACAGTGATCAGAGAGAGGCTGGGGTGTGTCTGTCCGGGACCCCCCTGCCTTCCTGC  
TCACCCTACTCTGACCTCCTTCACGTGCCAGGCCTGTGGGTAGTGGGGAGGGCTGAACAGGA  
CAACCTCTCATCACCTACTCTGACCTCCTTCACGTGCCAGGCCTGTGGGTAGTGGGGAGGG  
CTGAACAGGACAACCTCTCATCACCCCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAA



426/615

**FIGURE 422**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56531  
><subunit 1 of 1, 327 aa, 1 stop  
><MW: 37406, pI: 9.30, NX(S/T): 1  
MFPSRRKAAQLPWEDGRSGLLSGGLPRKCSVFHLFVACLSLGGFFSLLWLQLSCSGDVARAVRG  
QGQETSGPPRACPPPEPPPEHWEEDASWGPHRLAVLVPFRERFEELLVFVPHMRRFLSRKKIRH  
HIYVLNQVDHFRFNRAALINVGFLESSNSTDYIAMHDVDLLPLNEELDYGFPEAGPFHVASPE  
LHPLYHYKTYVGGILLLSKQHYRLCNGMSNRFWGWGREDDFYRRIKGAGLQLFRPSGITTGY  
KTRFRLHDPAWRKRDQKRIAAQKQEQFKVDREGGLNTVKYHVASRTALSVGGAPCTVLNIMLD  
CDKTATPWCTFS

**Signal peptide:**  
amino acids 1-42

**Transmembrane domain:**  
amino acids 29-49 (type II)

**N-glycosylation site.**  
amino acids 154-158

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**  
amino acids 27-31

**Tyrosine kinase phosphorylation site.**  
amino acids 226-233

**N-myristoylation site.**  
amino acids 19-25, 65-71, 247-253, 285-291, 303-309, 304-310

427/615

**FIGURE 423**

CCATCCCTGAGATCTTTTTATAAAAAACCCAGTCTTTGCTGACCAGACAAAGCATACCAGATC  
TCACCAGAGAGTCGCAGACACTATGCTGCCTCCCATGGCCCTGCCAGTGTGTCCTGGATGCT  
GCTTTCCTGCCTCATTCTCCTGTGTTCAGGTTCAAGGTGAAGAAACCCAGAAGGAAGTGCCTC  
TCCACGGATCAGCTGTCCCAAAGGCTCCAAGGCCTATGGCTCCCCCTGCTATGCCTTGTTTTT  
GTCACCAAATCCTGGATGGATGCAGATCTGGCTTGCCAGAAGCGGCCCTCTGGAAAAGTGGT  
GTCTGTGCTCAGTGGGGCTGAGGGATCCTTCGTGTCTCCTCCCTGGTGAGGAGCATTAGTAACAG  
CTACTCATACATCTGGATTGGGCTCCATGACCCACACAGGGCTCTGAGCCTGATGGAGATGG  
ATGGGAGTGGAGTAGCACTGATGTGATGAATTACTTTGCATGGGAGAAAAATCCCTCCACCAT  
CTTAAACCCTGGCCACTGTGGGAGCCTGTCAAGAAGCACAGGATTTCTGAAGTGGAAAGATTA  
TAACTGTGATGCAAAGTTACCCTATGTCTGCAAGTTCAAGGACTTAGGGCAGGTGGGAAGTCAG  
CAGCCTCAGCTTGGCGTGCAGCTCATCATGGACATGAGACCAGTGTGAAGACTCACCCTGGAA  
GAGAATATTCTCCCCAACTGCCCTACCTGACTACCTTGTGATGATCCTCCTTCTTTTTCCTT  
TTTCTTACCTTCATTTACAGGCTTTTCTGTCTTCCATGTCTTGAGATCTCAGAGAATAATA  
ATAAAATGTTACTTTATAAAAAAAAAAAAAAAAAAAAAA

428/615

**FIGURE 424**

&lt;/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56965

&lt;subunit 1 of 1, 175 aa, 1 stop

&lt;MW: 19330, pI: 7.25, NX(S/T): 1

MLPPMALPSVSWMLLSCLILLCQVQGEETQKELPSPRISCPKGSKAYGSPCYALFLSPKSWMD

ADLACQKRPSGKLVSVLSGAEGSFVSSLVRSISNSYSYIWIGLHDPTQGSEPDGDGWEWSSTD

VMNYFAWEKNPSTILNPGHCGSLSRSTGFLKWKDYNCDAKLPYVCKFKD

**Important features:****Signal peptide:**

amino acids 1-26

**C-type lectin domain signature.**

amino acids 146-171

429/615

**FIGURE 425**

CGGACGCGTGGGCGCCACCTCCGGAACAAGCCATGGTGGCGGCGACGGTGGCAGCGGCGTG  
CTGCTCCTGTGGGCTGCGGCCTGCGCGCAGCAGGAGCAGGACTTCTACGACTTCAAGGCGGTC  
AACATCCGGGGCAAACCTGGTGTGCTGGAGAAGTACCGCGGATCGGTGTCCCTGGTGGTGAAT  
GTGGCCAGCGAGTGCGGCTTCACAGACCAGCACTACCGAGCCCTGCAGCAGCTGCAGCGAGAC  
CTGGGCCCCCACCACCTTTAACGTGCTCGCCTTCCCCTGCAACCAGTTTGGCCAACAGGAGCCT  
GACAGCAACAAGGAGATTGAGAGCTTTGCCCGCCGCACCTACAGTGTCTCATTCCCCATGTTT  
AGCAAGATTGCAGTCACCGGTACTGGTGCCCATCCTGCCTTCAAGTACCTGGCCCAGACTTCT  
GGGAAGGAGCCCACCTGGAACCTTCTGGAAGTACCTAGTAGCCCCAGATGGAAAGGTGGTAGGG  
GCTTGGGACCCAACTGTGTCAGTGGAGGAGGTGAGACCCAGATCACAGCGCTCGTGAGGAAG  
CTCATCCTACTGAAGCGAGAAGACTTATTAACCACCGCGTCTCCTCCTCCACCACCTCATCCCG  
CCCACCTGTGTGGGGCTGACCAATGCAAACCTCAAATGGTGCTTCAAAGGGAGAGACCCACTGA  
CTCTCCTTCCTTTACTCTTATGCCATTGGTCCCATCATTCTTGTGGGGGAAAAATTCTAGTAT  
TTTGATTATTTGAATCTTACAGCAACAAATAGGAACTCCTGGCCAATGAGAGCTCTTGACCAG  
TGAATCACCAGCCGATACGAACGTCTTGCCAACAAAAATGTGTGGCAAATAGAAGTATATCAA  
GCAATAATCTCCCACCCAAGGCTTCTGTAAACTGGGACCAATGATTACCTCATAGGGCTGTTG  
TGAGGATTAGGATGAAATACCTGTGAAAGTGCCTAGGCAGTGCCAGCCAAATAGGAGGCATTC  
AATGAACATTTTTTGCATATAAACCAAAAAATAACTTGTTATCAATAAAAACTTGCATCCAAC  
ATGAATTTCCAGCCGATGATAATCCAGGCCAAAGGTTTAGTTGTTGTTATTTCTCTGTATTA  
TTTTCTTCATTACAAAAGAAATGCAAGTTCATTGTAACAATCCAAACAATACCTCACGATATA  
AAATAAAAATGAAAGTATCCTCCTCAAAA

430/615

**FIGURE 426**

MVAATVAAAWLLLWAAACAQQEQDFYDFKAVNIRGKLVSLVKYRGSVSLVVNVASECGFTDQH  
YRALQQQLQRDLGPHHFNVLAFFPCNQFGQQEPDSNKEIESFARRTYSVSFPMFSKIAVTGTGAH  
PAFKYLAQTSGKEPTWNFWKYL VAPDGKVVGAWDPTVSVEEVRPQITALVRKLILLKREDL

431/615

**FIGURE 427**

CAGTTCTGAAATCAATGGAGTTAATTTAGGGAATACAAACCAGCCATGGGGGTGGAGATTGCC  
TTTGCCTCAGTGATTCTCACCTGCCTCTCCCTTCTGGCAGCAGGAGTCTCCAGGTTGTTCTT  
CTCCAGCCAGTTCCAACCTCAGGAGACAGGTCCCAAGGCCATGGGAGATCTCTCCTGTGGCTTT  
GCCGGCCACTCATGAGAGTGTTTTTGTGTAAAGTATTTTTTAGAATACTGTTGACTTCTTCAT  
GATTTAATAACCATCCTTTGCGAAGTTTTATGAGGCTTTAGGGGAATGTCAACCCTCAAATTT  
TTGTTATACTAGATGGCTTCCATTTACCCACCACTATTTTAAGGTCCCTTTATTTTTAGGTTT  
AAGGTTCAATTTGACTTGAGAAAGTGCCCTTCTGCAGCTTCATTGATTTTGTTCCTTCACTA  
TTAATTGTAACGATTAAAAAGAATAAGAGCACGCAGACCTCTAGGAGAATATTTTATCCCTG  
GGTGCCCTGACACATTTATGTAGTGATCCCAAAATGTGATTGTTAATTTAAATGTTATTCT  
AATATTAGTACATTGAGTTGTGATGTAATATGAATAACCAGAATCTATTTCTTAAAGTTTTG  
AGTATATTTTCAACTAGATATTTGTATAGAAAGACTGAATAGTGATG

432/615

**FIGURE 428**

MGVEIAFASVILTCLSLAAGVSQVLLQPVPTQETGPKAMGDLSCGFAGHS

433/615

**FIGURE 429**

CCAAAGTGATCATTTGAAAAAGAGATATCCACATCTTCAAGCCCATATAAAGGATAGAAGCTG  
CACAGGGCAGCTTTACTTACTCCAGCACCTTCCTCTCCCAGGCAAATGGTGCTGACCATCTTT  
GGGATACAATCTCATGGATACGAGGTTTTTAACATCATCAGCCCAAGCAACAATGGTGGCAAT  
GTTCAGGAGACAGTGACAATTGATAATGAAAAAATAACCGCCATCGTTAACATCCATGCAGGA  
TCATGCTCTTCTACCACAATTTTTGACTATAAACATGGCTACATTGCATCCAGGGTGCTCTCC  
CGAAGAGCCTGCTTTATCCTGAAGATGGACCATCAGAACATCCCTCCTCTGAACAATCTCCAA  
TGGTACATCTATGAGAAACAGGCTCTGGACAACATGTTCTCCAACAAATACACCTGGGTCAAG  
TACAACCCTCTGGAGTCTCTGATCAAAGACGTGGATTGGTTCCTGCTTGGGTCACCCATTGAG  
AAACTCTGCAAACATATCCCTTTGTATAAGGGGGAAGTGGTTGAAAACACACATAATGTCGGT  
GCTGGAGGCTGTGCAAAGGCTGGGCTCCTGGGCATCTTGGGAATTTCAATCTGTGCAGACATT  
CATGTTTAGGATGATTAGCCCTCTTGTTTTATCTTTTCAAAGAAATACATCCTTGGTTTACAC  
TCAAAAGTCAAATTAAATTCTTTCCCAATGCCCCAACTAATTTTGAGATTCAAGTCAGAAAATA  
TAAATGCTGTATTTATA



434/615

**FIGURE 430**

><ss.DNA57834  
><subunit 1 of 1, 176 aa, 1 stop  
><MW: 19616, pI: 7.11, NX(S/T): 0  
MVLTIQSHGYEVFNIIISPSNNGGNVQETVTIDNEKNTAIVNIHAGSCSSTTIFDYKH  
GYIASRVLSRRACFILKMDHQNIPLNNLQWYIYEKQALDNMFSNKYTWVKYNPLESLIK  
DVDWFLGSPIEKLCKHIPLYKGEVVENTHNVGAGGCAKAGLLGILGISICADIHV

**Important features:****Signal peptide:**

Amino acids 1-26

**N-myristoylation sites:**

Amino acids 48-54;153-159;156-162;167-173

435/615

**FIGURE 431**

GCGTGGGGATGTCTAGGAGCTCGAAGGTGGTGGCTGGGCCTCTCGGTGCTGCTGACGGCGGCCA  
CAGTGGCCGGCGTACATGTGAAGCAGCAGTGGGACCAGCAGAGGCTTCGTGACGGAGTTATCA  
GAGACATTGAGAGGCCAAATTCGGAAAAAGAAAACATTCGTCTTTTGGGAGAACAGATTATTT  
TGACTGAGCAACTTGAAGCAGAAAGAGAGAAGATGTTATTGGCAAAAGGATCTCAAAAATCAT  
GACTTGAATGTGAAATATCTGTTGGACAGACAACACGAGTTTGTGTGTGTGTGTTGATGGAGA  
GTAGCTTAGTAGTATCTTCATCTTTTTTTTTTGGTCACTGTCCTTTTAACTTGATCAAATAAA  
GGACAGTGGGTCATATAAGTTACTGCTTTCAGGGTCCCTTATATCTGAATAAAGGAGTGTGGG  
CAGACACTTTTTTGAAGAGTCTGTCTGGGTGATCCTGGTAGAAGCCCCATTAGGGTCACTGTC  
CAGTGCTTAGGGTTGTTACTGAGAAGCACTGCCGAGCTTGTGAGAAGGAAGGGATGGATAGTA  
GCATCCACCTGAGTAGTCTGATCAGTCGGCATGATGACGAAGCCACGAGAACATCGACCTCAG  
AAGGACTGGAGGAAGGTGAAGTGGAGGGAGAGACGCTCCTGATCGTCGAATCC

436/615

**FIGURE 432**

MSRSSKVV LGLSVLLTAATVAGVHV KQWDQQLRDGVIRDIERQIRKKENIRLLGEQIILTE  
QLEAEREKMLLAKGSQKS

437/615

**FIGURE 433**

GAATTCGTGTCTCGGCACTCACTCCCGGCCGCCGGACAGGGAGCTTTCGCTGGCGCGCTTGGCCGGCGACAGGA  
CAGGTTCCGGGACGTCCATCTGTCCATCCGTCGGGAGAGAAATTACAGATCCGCAGCCCCGGGATGGGGCCGGCCC  
CGCTGCCGCTGCTGCTGGGCCCTTCTCTCCCCCGCTCTGGCGTAGAGCTATCACTGAGGCAAGGGAAGAAGCCA  
AGCCTTACCCGCTATTCCCGGGACCTTTTCCAGGGAGCCTGCAAACTGACCACACACCGCTGTTATCCCTTCCTC  
ACGCCAGTGGGTACCAGCCTGCCTTGATGTTTTACCAACCCAGCCTGGAAGACCACATACAGGAAACGTAGCCATT  
CCCCAGGTGACCTCTGTCAATCAAAGCCCTACCGCTCTTGCCCTCAAACACACAGTTGGACACATAATACTT  
TCTGAACATAAAGGTGTCAAATTTAATTGCTCAATCAATGTACCTAATATATACCAGGACACCACAATTTCTTGG  
TGGAAAGATGGGAAGGAATTGCTTGGGGGACATCATCGAATTACACAGTTTATCCAGATGATGAAGTTACAGCA  
ATAATCGCTTCCCTTCAGCATAACCAGTGTGCAGCGTTCAGACAATGGGTCGTATATCTGTAAGATGAAAATAAAC  
AATGAAGAGATCGTGTCTGATCCCATCTACATCGAAGTACAAGGACTTCCCTCACTTTACTAAGCAGCCTGAGAGC  
ATGAATGTCAACAGAAACACAGCCTTCAACCTCACCTGTGAGGCTGTGGGCCCGCTGAGCCCGTCAACATTTTC  
TGGGTTCAAACAGTAGCCGTGTTAACGAACAGCCTGAAAAATCCCCGGCGTGCTAACTGTTCCAGGCCTGACG  
GAGATGGCGGTCTTCAGTTGTGAGGCCCACAATGACAAAGGGCTGACCGTGTCCAGGGAGTGAGATCAACATC  
AAAGCAATTCCTCCCCACCACTGAAGTCAGCATCCGTAACAGCACTGCACACAGCATTCTGATCTCCTGGGTT  
CCTGGTTTTGATGGATACTCCCGTTGAGGAATTGCGACATTGAGGTCAAGGAAGCTGATCCGCTGGGTAATGGC  
TCAGTCATGATTTTTAACACCTCTGCCTTACCACATCTGTACCAATCAAGCAGCTGCAAGCCCTGGCTAATTAC  
AGCATTGGTGTTCCTGCATGAATGAAATAGGCTGGTCTGCAGTGAGCCCTTGGATTCTAGCAAGCAGCACTGAA  
GGAGCCCCATCAGTAGCACCTTTAAATGTCACTGTGTTTCTGAATGAATCTAGTGATAATGTGGACATCAGATGG  
ATGAAGCCTCCGACTAAGCAGCAGGATGGAGAATGGTGGGCTACCGGATATCCACGTTGGCAGAGTGACAGGG  
ATTTCCAAAGAGCTCTTGGAGGAAGTTGGCCAGAATGGCAGCCGAGCTCGGATCTCTGTTCAAGTCCACAATGCT  
ACGTGCACAGTGAGGATTGCAGCCGTACCCAGAGGGGGAGTTGGGCCCTTCAGTGATCCAGTGAAGAAATTTTATC  
CCTGCACACGGTTGGGTAGATTATGCCCCCTCTTCAACTCCGGCGCTGGCAACGCAGATCCTGTGCTCATCATC  
TTTGGCTGCTTTTGTGGATTTATTTTGATTGGGTTGATTTTATACATCTCCTTGGCCATCAGAAAAAGAGTCCAG  
GAGACAAAGTTTGGGAATGCATTACAGAGGAGGATTCTGAATTAGTGGTGAATTATATAGCAAAAGAAATCCTTC  
TGTCGGCGAGCCATTGAACCTACCTTACATAGCTTGGGAGTCAGTGAGGAACACAAAATAAAGTAGAAGATGTT  
GTGATTGACAGGAATCTTCTAATTCTTGGAAAAATTCTGGGTGAAGGAGAGTTTGGGTCTGTAATGGAAGGAAT  
CTTAAGCAGGAAGATGGGACCTCTCTGAAAGTGGCAGTGAAGACCATGAAGTTGGACAACCTTTCACATCGGGAG  
ATCGAGGAGTTTCTCAGTGAGGCAGCGTCATGAAAGACTTCAGCCACCCAAATGTCACTCGACTTCTAGGTGTG  
TGTATAGAAATGAGCTCTCAAGGCATCCCAAGGCCCATGGTAATTTTACCCTTCATGAAATACGGGGACCTGCAT  
ACTTACTTACTTTATTTCCGATTGGAGACAGGACCAAGCATATTCCTCTGCAGACACTATTGAAGTTTCATGGTG  
GATATTGCCCTGGGAATGGAGTATCTGAGCAACAGGAATTTTCTTCATCGAGATTTAGCTGCTCGAAACTGCATG  
TTGCGAGATGACATGACTGTCTGTGTGCGGACTTCGGCCTCTCTAAGAAGATTTACAGTGCGGATTATTACC  
CAAGGCCGATGCTAAGATGCCTGTTAAATGGATCGCCATAGAAAGTCTTGCAGACCGAGTCTACACAAGTAA  
AGTGATGTGTGGGCATTTGGCGTGACCATGTGGGAAATACGTACGCGGGGAATGACTCCCTATCCTGGGGTCCAG  
AACCATGAGATGTATGACTATCTTCTCCATGGCCACAGGTTGAAGCAGCCCCGAAGACTGCCTGGATGAAGTGTAT  
GAAATAATGTACTCTTGTGGAGAACCGATCCCTTAGACCGCCCCACCTTTTTCAGTATTGAGGCTGCAGCTAGAA  
AAACTCTTAGAAAGTTTGCCTGACGTTCCGAACCAAGCAGACGTTATTTACGTCAATACACAGTTGCTGGAGAGC  
TCTGAGGCGCTGGCCAGGGCCCCACCCTTGTCTCACTGGACTTGAACATCGACCCCTGACTCTATAATTGCCTCC  
TGCACTCCCCGCGCTGCCATCAGTGTGGTCACAGCAGAAAGTTTCATGACAGCAACCTCATGAAGGACGGTACATC  
CTGAATGGGGGAGTGAGGAATGGGAAGATCTGACTTCTGCCCCCTCTGCTGCAGTCACAGCTGAAAAGAACAGT  
GTTTTACCGGGGAGAGACTTGTTAGGAATGGGGTCTCCTGGTCCCATTCGAGCATGCTGCCCTTGGGAAGCTCA  
TTGCCGATGAACTTTTGTTTGTGACGACTCCTCAGAAGGCTCAGAAGTCTGATGTGAGGAGAGGTGCGGGGA  
GACATTCAAAAATCAAGCCAATTCTTCTGCTGTAGGAGAATCCAATTGTACCTGATGTTTTTGGTATTGTCTT  
CCTTACCAAGTGAACCTCATGGCCCCAAAGCACCAGATGAATGTTGTTAAGGAAGCTGTCAATAAAAATACATAA  
TATATATTTATTTAAAGAGAAAAATATGTGTATATCATGAAAAAGACAAGGATATTTTAAATAAACATTACTTA  
TTTCATTTCACTTATCTTGCATATCTTAAATTAAGCTTCAGCTGCTCCTTGATATTAACTTTGTACAGAGTTG  
AAGTTGTTTTTCAACTTCTTTTCTTTTCTTACTATTAATGTAAAAATATTTGTAATAATGAAATGCCATATT  
TGACTTGGCTTCTGGTCTTGATGATTTGATAAGAATGATTAATTTTCTGATATGGCTCCATAATAAAATGAA  
ATAGGA

438/615

**FIGURE 434**

MGPAPLPLLLGLFLPALWRRRAITEAREEAKPYPLFPFPFPGSLQTDHTPLLSLPHASGYQPALMFSPTQGRPH  
 GNVAIPQVTSVESKPLPPLAFKHTVGHIIILSEHKGVKFNC SINVPNIYQD TTISWWKDGKELLGGHHRITQFY  
 DEVTAAIIASF SITSVQRSDNGSYICKMKINNEEIVSDPIYIEVQGLPHFTKQPE SMNVTRNTAFNLTCQAVGP  
 PVNIFWVQNSSRVNEQPEKSPGVLTVPGLTEMAVFSCEAHNDKGLTVSQGVQINIKAI PPSPTTEVSIRNSTAHS  
 LISWVPGFDGYS PFRNC SIQVKEADPLGNGSVMIFNTSALPHLYQIKQLQALANYSIGVSCMNEIGWSAVSPWIL  
 ASTTEGAPSVAPLNVTVFLNESSDNVDIRWMKPPTKQD GELVGYRISHVWQSAGISKELLEEVGQNGSRARISV  
 QVHNATCTVRIA AVTRGGVGPFS DPVKIFIPAHGWVDYAPSSTPAPGNADPVLIIFGCFCGFILIGLILYISLAI  
 RKRVTQETKFGNAFTEEDSELVVNYIAKKSFCRRAIELTLHSLGVSEELQNKLEDVVIDRNL LILGKILGEGEFGS  
 VMEGNLKQEDGTS LKVAVKTMKLDNSSHREIEEFLSEAACMKDFSHPNVIRLLGVCIEMSSQGI PKPMVILPFMK  
 YGDLHTYLLYSRLETGPKHIPLQTL LKFMVDIALGMEYLSNRNFLHRDLAARNCMLRDDMTVCVADFGLSKKIYS  
 GDYYRQGRIAKMPVKWIAIESLADRVYTSKSDVWAFGV TMWEIRTRGMT PYPGVQNH EMYDYLLHGHRLKQPEDC  
 LDELYEIMYSCWR TDPLDRPTFSVLR LQLEKLLSLPDVNRQADVIVNTQLLESSEGLAQGPTLAPLDLNI DPD  
 SIIASCTPRAAISVVTAEVHDSKPHEGRYIILNGGSEEWEDLTSAPSAAVTAEKNSVLPGERLVRNGVSWSHSSML  
 PLGSSLPDELLFADDSSEGSEVL M

Signal sequence:	Amino acids 1-18
Transmembrane domain:	Amino acids 501-520
N-glycosylation sites:	Amino acids 114-118;170-174;207-211; 215-219;234-238;294-298;316-320;329-333; 336-340;354-358;389-393;395-399;442-446; 454-458;625-629
Tyrosine kinase phosphorylation sites:	Amino acids 675-683;865-873;923-930
N-myristoylation sites:	Amino acids 41-47;110-116;171-177; 269-275;275-281;440-446;507-513;535-541; 966-972
Prokaryotic membrane lipoprotein lipid attachment site:	Amino acids 351-362
Tyrosine protein kinases specific active-site signature:	Amino acids 719-732

439/615

**FIGURE 435**

AATGTGAGAGGGGCTGATGGAAGCTGATAGGCAGGACTGGAGTGTTAGCACCAGTACTGGATG  
TGACAGCAGGCAGAGGAGCACTTAGCAGCTTATTCAGTGTCCGATTCTGATTCCGGCAAGGAT  
CCAAGCATGGGAATGCTGCCGTGCGGCAACTCCTGGCACACTGCTCCTCTTTCTGGCTTTCTTG  
CTCCTGAGTTCCAGGACCGCACGCTCCGAGGAGGACCGGGACGGCCTATGGGATGCCTGGGGC  
CCATGGAGTGAATGCTCACGCACCTGCGGGGGAGGGGCCTCCTACTCTCTGAGGCGCTGCCTG  
AGCAGCAAGAGCTGTGAAGGAAGAAATATCCGATACAGAACATGCAGTAATGTGGACTGCCCA  
CCAGAAGCAGGTGATTTCCGAGCTCAGCAATGCTCAGCTCATAATGATGTCAAGCACCATGGC  
CAGTTTTATGAATGGCTTCCTGTGTCTAATGACCCTGACAACCCATGTTCACTCAAGTGCCAA  
GCCAAAGGAACAACCCTGGTTGTTGAACTAGCACCTAAGGTCTTAGATGGTACGCGTTGCTAT  
ACAGAACTCTTTGGATATGTGCATCAGTGGTTTTATGCCAAATTGTTGGCTGCGATCACCAGCTG  
GGAAGCACCGTCAAGGAAGATAACTGTGGGGTCTGCAACGGAGATGGGTCCACCTGCCGGCTG  
GTCCGAGGGCAGTATAAATCCCAGCTCTCCGCAACCAAATCGGATGATACTGTGGTTGCACTT  
CCCTATGGAAGTAGACATATTCGCCTTGTCTTAAAGGTCTGATCACTTATATCTGGAAACC  
AAAACCCTCCAGGGGACTAAAGGTGAAAACAGTCTCAGCTCCACAGGAACCTTTCCTTGTGGAC  
AATTCTAGTGTGGACTTCCAGAAATTTCCAGACAAAGAGATACTGAGAATGGCTGGACCACTC  
ACAGCAGATTTTATTGTCAAGATTTCGTAACCTCGGGCTCCGCTGACAGTACAGTCCAGTTCATC  
TTCTATCAACCCATCATCCACCGATGGAGGGAGACGGATTTCTTTCCTTGCTCAGCAACCTGT  
GGAGGAGGTTATCAGCTGACATCGGCTGAGTGCTACGATCTGAGGAGCAACCGTGTGGTTGCT  
GACCAATACTGTCACTATTACCCAGAGAACATCAAACCCAAACCCAAGCTTCAGGAGTGCAAC  
TTGGATCCTTGTCCAGCCAGTGACGGATACAAGCAGATCATGCCTTATGACCTCTACCATCCC  
CTTCCTCGGTGGGAGGCCACCCCATGGACCGCGTGCTCCTCCTCGTGTGGGGGGGCATCCAG  
AGCCGGGCAGTTTCCTGTGTGGAGGAGGACATCCAGGGGCATGTCACCTCAGTGGAAGAGTGG  
AAATGCATGTACACCCCTAAGATGCCCATCGCGCAGCCCTGCAACATTTTTGACTGCCCTAAA  
TGGCTGGCACAGGAGTGGTCTCCGTGCACAGTGACATGTGGCCAGGGCCTCAGATACCGTGTG  
GTCTCTGCATCGACCATCGAGGAATGCACACAGGAGGCTGTAGCCCAAAACAAAGCCCCAC  
ATAAAAGAGGAATGCATCGTACCCACTCCCTGCTATAAACCCAAAGAGAACTTCCAGTCGAG  
GCCAAGTTGCCATGGTTCAAACAAGCTCAAGAGCTAGAAGAAGGAGCTGCTGTGTCAGAGGAG  
CCCTCGTAAAGTTGTAAAGCACAGACTGTTCTATATTTGAACTGTTTTGTTTAAAGAAAGCA  
GTGTCTCACTGGTTGTAGCTTTCATGGGTTCTGAACTAAGTGTAATCATCTCACCAAAGCTTT  
TTGGCTCTCAAATTAAAGATTGATTAGTTTCAAAAAAAAAA

440/615

**FIGURE 436**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58847  
<subunit 1 of 1, 525 aa, 1 stop  
<MW: 58416, pI: 6.62, NX(S/T): 1  
MECCRRATPGTLLLFLAFLLLSSRTARSEEDRDGLWDAWGPWSECSRTC GGGASYSLRRCLSS  
KSCEGRNIRYRTCSNVDCPPEAGDFRAQQCSAHNDVKHHGQFYEWLPVSNPDNPCSLKCQAK  
GTTLVVELAPKVLDGTRCYTESLDMCISGLCQIVGCDHQLGSTVKEDNCGVCNGDGSTCRLVR  
GQYKSQLSATKSDDTVVALPYGSRHIRLVLKGPDLHLYLETKTLQGTKGENSLSSSTGTFLVDNS  
SVDFQKFPDKEILRMAGPLTADFIVKIRNSGSADSTVQFIFYQPIIHRWRETDFFPSCATCGG  
GYQLTSAECYDLRSNRVVADQYCHYYPENIKPKPKLQECNLDP CPASDGYKQIMPYDLYHPLP  
RWEATPWTACSSSCGGGIQSRAVSCVEEDIQGHVTSVEEWKCMYTPKMPIAQPCNIFDCPKWL  
AQEWSPTVTCGQGLRYRVVLCIDHRGMHTGGCSPKTKPHIKEECIVPTPCYKPKEKLPVEAK  
LPWFKQAQELEEAAVSEEPS

**Important features:****Signal peptide:**

amino acids 1-25

**N-glycosylation site.**

amino acids 251-254

**Thrombospondin 1**

amino acids 385-399

**von Willebrand factor type C domain proteins**

amino acids 385-399, 445-459 and 42-56

441/615

**FIGURE 437**

AACTGGAAGGAAAGAAAGAAAGGTCAGCTTTGGCCCAGATGTGGTTACCCCTTGGTCTCCTGT  
CTTTATGTCTTTCTCCTCTTCCTATTCTGTCTATCTCCCTCACTTAAGTCTCAGGCCTGTCAGC  
AGCTCCTGTGGACATTGCCATCCCCCTCTGGTAGCCTTCAGAGCAAACAGGACAACCTATGTTA  
TGGATGTTTCCACCAACCAGGGTAGTGGCATGGAGCACCGTAACCATCTGTGCTTCTGTGATC  
TCTATGACAGAGCCACTTCTCCACCTCTGAAATGTTCCCTGCTCTGAATCTGGCATGAGATG  
GCACAGGTGACCACGCAGAAGCCACCAGAATCTTGCCTGCCCTATTCCTCCTCCCAAGTCTGT  
TCTCTTATTGTCAACCTCAGCACAAACAGGCTGGCGCCAATGGCATTACAGAGAAAGCAATCTG  
TGTGGCTAGTGGGCAGATTACCATGCAAGCCCCAGGAGAAATGGAGGAGCTTTGTAGCCACCT  
CCCTGTCAGCCAGTATTAACATGTCCCCTTCCCCCTGCCCCGCCGTAGATTACAGGACATTCGC  
CCCTGTGTGCCACCAAACCAGGACTTTCCCCTTGGCTTGGCATCCCTGGCTCTCTCCTGGTAC  
CCAGCAAGACGTCTGTTCCAGGGCAGTGTAGCATCTTTCAAGCTCCGTTACTATGGCGATGGC  
CATGATGTTACAATCCCCTTGCCTGAATAATCAAGTGGGAAGGGGAAGCAGAGGGAAATGGG  
GCCATGTGAATGCAGCTGCTCTGTTCTCCCTACCCTGAGGAAAAACCAAAGGGGAAGCAACAGG  
AACTTCTGCAACTGGTTTTTATCGGAAAGATCATCCTGCCTGCAGATGCTGTTGAAGGGGCAC  
AAGAAATGTAGCTGGAGAAGATTGATGAAAGTGCAGGTGTGTAAGGAAATAGAACAGTCTGCT  
GGGAGTCAGACCTGGAATTCTGATTCCAACTCTTTATTACTTTGGGAAGTCACTCAGCCTCC  
CCGTAGCCATCTCCAGGGTGACGGAACCCAGTGTATTACCTGCTGGAACCAAGGAAACTAACA  
ATGTAGGTACTAGTGAATACCCAATGGTTTCTCCAATTATGCCCATGCCACCAAAACAATA  
AAACAAAATTCTCTAACACTGAAA



WO 01/68848

PCT/US01/06520

442/615

**FIGURE 438**

MWLPLGLLSLCLSPILSSPSLKSQACQQLLWTLPSPLVAFRANRTTYVMDVSTNQSGMEH  
RNHLCFCDLYDRATSPPLKCSLL

443/615

**FIGURE 439**

GTTCCTCATAGTTGGCGTCTTCTAAAGGAAAAACACTAAAATGAGGAACCTCAGCGGACCGGGAGCGACGCAGCTT  
GAGGGAAGCATCCCTAGCTGTTGGCGCAGAGGGGCGAGGCTGAAGCCGAGTGGCCCCGAGGTGTCTGAGGGGCTGG  
GGCAAAGGTGAAAGAGTTTTCAGAACAAAGCTTCTGGAACCCATGACCCATGAAGTCTTGTGACATTTATACCGT  
CTGAGGGTAGCAGCTCGAAACTAGAAGAGTGGAGTGTGGCAGGGACGGCAGTATCTCTTTGTGTGACCCCTGGC  
GGCCTATGGGACGTTGGCTTCAGACCTTTGTGATACCACTAGCTGCGTGGGACGATGACGGCGTGGAGAGGAATG  
AGGCCTGAGGTCACACTGGCTTGCTCCTCTAGCCACAGCAGGCTGCTTTGCTGACTTGAACGAGGTCCCTCAG  
GTCACCGTCCAGCCTGCGTCCACCGTCCAGAAGCCCGGAGGCACTGTGATCTTGGGCTGCGTGGTGAACCTCCA  
AGGATGAATGTAACCTGGCGCCTGAATGGAAGGAGCTGAATGGCTCGGATGATGCTCTGGGTGTCTCATCACC  
CACGGGACCCCTCGTCATCACTGCCCTTAACAACCCACACTGTGGGACGGTACCAGTGTGTGGCCCGGATGCCCTGCG  
GGGGCTGTGGCCAGCGTGCCAGCCACTGTGACACTAGCCAATCTCCAGGACTTCAAGTTAGATGTGCAGCACGTG  
ATTGAAGTGGATGAGGGAACACAGCAGTCAATGGCTGCCACCTGCCGTGAGAGCCACCCCAAGCCAGGTCCGG  
TACAGCGTCAAACAAGAGTGGCTGGAGGCCCTCAGAGGTAACCTACCTGATCATGCCCTCAGGGAACCTCCAGATT  
GTGAATGCCAGCCAGGAGGACGAGGGCATGTACAGTGTGCAGCCTACAACCCAGTACCCAGGAAGTGAAACCC  
TCCGGCTCCAGCGACAGGCTACGTGTGGCGCGCTCCACCGCTGAGGCTGCCCGCATCATCTACCCCCAGAGGCC  
CAAACCATCATCGTCACCAAAGGCCAGAGTCTCATTTGAGAGTGTGTGGCCAGTGAATCCACCCCCAGGGTCC  
ACCTGGGCCAAGGATGGGTCCAGTGTACCGGCTCACAAGTGTGACGCGCTTCCCTGCTGAGCAACCTCCTCATCGAC  
ACCACGAGCGAGGAGGACTCAGGCACCTACCGCTGCATGGCCGACAATGGGGTTGGGCAGCCCGGGGAGCGTCC  
ATCCTCTACAATGTCCAGGTGTTTGAACCCCTGAGGTACCATGGAGCTATCCAGCTGGTTCATCCCTGGGGC  
CAGAGTGCCAAGCTTACCTGTGAGGTGCGTGGGAACCCCGCCCTCCGTGCTGTGGTGTGAGGAATGCTGTGCCC  
CTCATCTCCAGCCAGCGCCTCCGGCTCTCCCGCAGGGCCCTGCGCGTGTCTAGCATGGGGCCTGAGGACGAGGC  
GTCTACCAGTGCATGGCCGAGAACGAGGTTGGGAGCGCCCATGCCGTAGTCCAGCTGCGGACCTCCAGGCCAAGC  
ATAACCCCAAGGCTATGGCAGGATGCTGAGCTGGCTACTGGCACACCTCCTGTATCACCTCCAAACTCGGCAAC  
CCTGAGCAGATGCTGAGGGGGCAACCGGGCTCCCGAGACCCCAACGTGAGTGGGGCTGCTTCCCGAAGTGT  
CCAGGAGAGAAGGGGAGGGGGCTCCCGCCGAGGCTCACCAGTATCCTCAGCTCGCCCGCACCTCCAGACAGAC  
TCATATGAAGTGTGTGGCGGCTCGGCATGAGGGCAGTGGCCGGGCGCCAATCCTCTACTATGTGGTGAACAC  
CGCAAGCAGGTACAAATTCCTCTGACGATTGGACCATCTCTGGCATTCACGCCAACCCAGCACCGCCTGACCCCTC  
ACCAGACTTGACCCCGGGAGCTTGTATGAAGTGGAGTGGCAGCTTACAACCTGTGCGGGAGAGGGCCAGACAGCC  
ATGGTCACCTTCCGAAGTGGACGGCGGCCCAACCCGAGATCATGGCCAGCAAGAGACAGCAGATCCAGAGAGAC  
GACCTTGGAGCCAGTCCCGAGAGCAGCAGCCAGCCAGACCGCCGCTCTCCCCCAGAAGCTCCCGACAGG  
CCCACCATCTCCACGGCCTCCGAGACCTCAGTGTACGTGACCTGGATTCCCCGTGGGAATGGTGGGTTCCTAATC  
CAGTCCCTTCCGTGTGGAGTACAAGAAGCTAAAGAAAGTGGGAGACTGGATTCTGGCCACCGCCATCCCCCA  
TCGCGGCTGTCCGTGGAGATCACGGGCTAGAGAAAGGCACCTCCTACAAGTTTCGAGTCCGGGCTCTGAACATG  
CTGGGGGAGAGCGAGCCAGCGCCCCCTCTCGGCCCTACGTGGTGTGCGGCTACAGCGGTGCGGTGTACGAGAGG  
CCCGTGGCAGGTCTTATATACCTTACGGATGCGGTCAATGAGACCACCATCATGCTCAAGTGGATGTACATC  
CCAGCAAGTAACAACAACACCCCAATCCATGGCTTTTATATCTATTATCGACCCACAGACAGTCAATGATAGT  
GACTACAAGAAGGATATGGTGAAGGGGACAAGTACTGGCACTCCATCAGCCACCTGCAGCCAGAGACCTCCTAC  
GACATTAAGATGCAGTGTTCATGAAGGAGGGGAGAGCGAGTTTCAAGCAACGTGATGATCTGTGAGACCAAGCT  
CGGAAGTCTTCTGGCCAGCCTGGTGCAGTGCACCCCAACTCTGGCCCCACCACAGCCGCCCCCTTCTGAAACC  
ATAGAGCGGCGCGTGGGCACCTGGGGCCATGGTGGCTCGCTCCAGCGACCTGCCCTATCTGATTGTGCGGGTCTG  
CTGGGCTCCATCGTTCTCATCATCGTCACTTCTATCCCTTCTGCTTGTGGAGGGCCTGGTCTAAGCAAAACAT  
ACAACAGACCTGGGTTTTCTCGAAGTGCCCTTCCACCCCTCCTGCCGTATACTATGGTGCCATTGGGAGGACTC  
CCAGGCCACCCAGCCAGTGGACAGCCCTACCTCAGTGGCATCAGTGGACGGGCTGTGCTAATGGGATCCACATG  
AATAGGGGCTGCCCCCTCGGCTGCAGTGGGCTACCCGGGCATGAAGCCCCAGCAGCACTGCCAGGCGAGCTTCA  
CAGCAGAGTGACACCAGCAGCCTGCTGAGGCAGACCCATCTTGGCAATGGATATGACCCCAAGTACCAGATC  
ACGAGGGGTCCCAAGTCTAGCCCGACGAGGGCTCTTTCTTATACACACTGCCCCGACGACTCCACTCACCAGCTG  
CTGCAGCCCCATCACGACTGCTGCCAACGCCAGGAGCAGCCTGCTGCTGTGGGCCAGTCAGGGGTGAGGAGAGCC  
CCCGACAGTCTGTCTTGAAGCAGTGTGGGACCTCCATTTCACTCAGGGCCCCCATGCTGCTTGGGCCTTGTG  
CCAGTTGAAGAGGTGGACAGTCTGACTCCTGCCAAGTGAAGTGGAGGAGTGGTGTCCCAGCACCCCGTAGGG  
GCCTACGTAGGACAGGAACCTGGAATGCAGCTCTCCCGGGGCCACTGGTGGTGTGCTTTTGAACACCACT  
CTCACAAATTAGGCAGAAGCTGATATCCAGAAAGACTATATATTGTTTTTTTTTAAAAAAGAGAAAAA  
AGAGACAGAGAAAAATTGGTATTTATTTTCTATTATAGCCATATTTATATATTTATGCACTTGTAAATAAATGTA  
TATGTTTTATAATTCTGGAGAGACATAAGGAGTCTACCCGTTGAGGTTGGAGAGGGAAAAATAAAGAAGCTGCCA  
CCTAACAGGAGTCAACCAGGAAAGCACCGCACAGGCTGGCGCGGGACAGACTCCTAACCTGGGGCCTCTGCAGTG  
GCAGGCGAGGCTGCAGGAGGCCACAGATAAGCTGGCAAGAGGAAGGATCCAGGCACATGGTTCATCAGCAGCA  
TGAGGGAACAGCAAGGGGCACGGTATCACAGCCTGGAGACACCCACACAGATGGCTGGATCCGGTGTACGGGAA  
ACATTTTCTAAGATGCCCATGAGAACAGACCAAGATGTGTACAGCACTATGAGCATTAAAAACCTTCCAGAAT  
CAATAATCCGTGGAACATATCTCTGTAAAAACAACACTGTAACCTCTAAATAAATGTTTAGTCTTCCCTGTAAAA

444/615

**FIGURE 440**

MLRGTMTAWRGMRPEVTLACLLLATAGCFADLNEVPQVTVQPASTVQKPGGTVILGCVVEPPR  
MNVTWRLNGKELNGSDDALGVLITHGTLVITALNNHTVGRYQCVARMPAGAVASVPATVTLAN  
LQDFKLDVQHVIEVDEGNTAVIACHLPESHKPAQVRYSVKQEWLEASRGNYLIMP SGNLQIVN  
ASQEDEGMYKCAAYNPVTQEVKTSGSSDRLRVRRTAEAAARI IYPPEAQTIIVTKGQSLILEC  
VASGIPPPRVTWAKDGSSVTGYNKTRFLLSNLLIDTTSEEDSGTYRCMADNGVQPGA AVILY  
NVQVFEPPEVTMELS QLVI PWGQSAKLTCEVRGNPPPSVLWLRNAVPLISSQRLRLSRRALRV  
LSMGPEDEGVYQCAENEVGSAAHAVVQLRTSRPSITPRLWQDAELATGTPPVSPSKLGNPEQM  
LRGQPALPRPPTSVGPASPKCPGEGKGQGA PAEAPIILSSPRTSKTDSYELVWRPRHEGSGRAP  
ILYYVVKHRKQVTNSSDDWTISGIPANQHRLTLTRLDPGSLYEVEMAAYNCAGEGQTAMVTFR  
TGRRPKPEIMASKEQQIQRDDPGAS PQSSSQPDHGRLSPPEAPDRPTISTASETSVYVTWIPR  
GNGGFPIQSFRVEYKKLKKVGDWILATSAIPPSRLSVEITGLEKGT SYKFRVRALNMLGESEP  
SAPSRPYVVS GYSGRVYERP VAGPYITFTDAVNETTIMLKWMIIPASNNNTPIHGFYIYYRPT  
DSDNDSYKKDMVEGD KYWHSISHLQPETSYDIKMOCFNEGGESEFSNVMICETKARKSSGQP  
GRLPPPTLAPPQPPLPETIERPVGTGAMVARSSDLPYLIVGVVLGSI VLIIVTFIPFCLWRAW  
SKQKHTTDLGFPR SALPPSCPYTMVPLGGLPGHQASGQPYLSGISGRACANGIHMNRGCPSAA  
VGYPGMKPQQHCPGELQQQSDTSSLLRQTHLGNGYDPQSHQITRGPKSSPDEGSFLYTL PDDS  
THQLLQPHHDCCQRQE QPAAVGQSGVRRAPDSPVLEAVWDPPFHSGPPCCLGLVPVEEVDSPD  
SCQVSGGDWCPQHVP GAYVGQEPGMQLSPGPLVRVSFETPPLTI

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 16-30 (type II), 854-879

445/615

**FIGURE 441**

GAGAGAATAGCTACAGATTCTCCATCCTCAGTCTTTGCAAGGCGACAGCTGTGCCAGCCGGGC  
TCTGGCAGGCTCCTGGCAGCATGGCAGTGAAGCTTGGGACCCTCCTGCTGGCCCTTGCCCTGG  
GCCTGGCCCAGCCAGCCTCTGCCCCGCCGGAAGCTGCTGGTGTCTCTGCTGGATGGTTTTCTGCT  
CAGACTACATCAGTGATGAGGCGCTGGAGTCATTGCCTGGTTTTCAAAGAGATTGTGAGCAGGG  
GAGTAAAAGTGGATTACTTGACTCCAGACTTCCCTAGTCTCTCGTATCCCAATTATTATACCC  
TAATGACTGGCCGCCATTGTGAAGTCCATCAGATGATCGGGAACCTACATGTGGGACCCACCA  
CCAACAAGTCCTTTGACATTGGCGTCAACAAAGACAGCCTAATGCCTCTCTGGTGGGAATGGAT  
CAGAACCTCTGTGGGTCACTCTGACCAAGGCCAAAAGGAAGGTCTACATGTACTACTGGCCAG  
GCTGTGAGGTTGAGATTCTGGGTGTGAGACCCACCTACTGCCTAGAATATAAAAATGTCCCAA  
CGGATATCAATTTTGCCAATGCAGTCAGCGATGCTCTTGACTCCTTCAAGAGTGGCCGGGCCG  
ACCTGGCAGCCATATACCATGAGCGCATTGACGTGGAAGGCCACCCTACGGGCCTGCATCTG  
CGCAGAGGAAAGATGCCCTCAAGGCTGTAGACACTGTCCTGAAGTACATGACCAAGTGGATCC  
AGGAGCGGGGCTGCAGGACCGCCTGAACGTCATTATTTCTCGGATCACGGAATGACCGACA  
TTTTCTGGATGGACAAAGTGATTGAGCTGAATAAGTACATCAGCCTGAATGACCTGCAGCAAG  
TGAAGGACCGCGGGCCTGTTGTGAGCCTTTGGCCGGCCCCCTGGGAAACACTCTGAGATATATA  
ACAACTGAGCACAGTGGAACACATGACTGTCTACGAGAAAGAAGCCATCCCAAGCAGGTTCT  
ATTACAAGAAAGGAAAGTTTGTCTCTCCTTTGACTTTAGTGGCTGATGAAGGCTGGTTTCATAA  
CTGAGAATCGAGAGATGCTTCCGTTTTGGATGAACAGCACCGGCAGGCGGGAAGGTTGGCAGC  
GTGGATGGCACGGCTACGACAACGAGCTCATGGACATGCGGGGCATCTTCCTGGCCTTCGGAC  
CTGATTTCAAATCCAACTTCAGAGCTGCTCCTATCAGGTCGGTGGACGTCTACAATGTCATGT  
GCAATGTGGTGGGCATCACCCCGCTGCCCAACAACGGATCCTGGTCCAGGGTGATGTGCATGC  
TGAAGGGCCGCGCCGGCACTGCCCCGCCTGTCTGGCCCAGCCACTGTGCCCTGGCACTGATTC  
TTCTCTTCCTGCTTGCATAACTGATCATATTGCTTGTCTCAGAAAAAACACCATCAGCAAAG  
TGGGCCTCCAAAGCCAGATGATTTTCATTTTATGTGTGAATAATAGCTTCATTAACACAATCA  
AGACCATGCACATTGTAAATACATTATTCTTGGATAATTCTATACATAAAAGTTCCTACTTGT  
TAAA

446/615

**FIGURE 442**

MAVKLGTTTTLLALALGLAQPASARRKLLVFLLDGFERSDYISDEALES LPGFKEIVSRGVKVDYL  
TPDFPSLSYPNYYTLMTGRHCEVHQMIGNYMWDPTTNKSF DIGVNKDSL MPLWNGSEPLWVT  
LTKAKRKVYMYWPGCEVEILGVRPTYCLEYKNVPTDINFANAVSDALDSFKSGRADLA AIYH  
ERIDVEGHHYGPASPQRKDALKAVDTVLKYMTKWIQERGLQDRLNVIIFSDHGMTDIFWMDKV  
IELNKYISLNDLQQVKDRGPVVS LWPAPGKHSEIYNKLSTVEHMTVYEKEAIPSRFYKKGKF  
VSPLTLVADEGWFITENREMLPFWMNSTGRREGWQRGWHGYDNELMDMRGIFLAFGPDFKSNF  
RAAPIRSVDVYNVMCNVVGITPLPNNGSWSRVMCMLKGRAGTAPPVWPSHCALALILLFLLA

**Important features of the protein:****Signal peptide:**

amino acids 1-22

**N-glycosylation sites.**

amino acids 100-104, 118-122, 341-345, 404-408

**N-myristoylation sites.**

amino acids 148-154, 365-371

**Amidation site.**

amino acids 343-347

447/615

**FIGURE 443**

AGTGACTGCAGCCTTCCTAGATCCCCTCCACTCGGTTTCTCTCTTTGCAGGAGCACCGGCAGC  
ACCAGTGTGTGAGGGGAGCAGGCAGCGGTCTAGCCAGTTCCTTGATCCTGCCAGACCACCCA  
GCCCCCGGCACAGAGCTGCTCCACAGGCACCATGAGGATCATGCTGCTATTACAGCCATCCT  
GGCCTTCAGCCTAGCTCAGAGCTTTGGGGCTGTCTGTAAGGAGCCACAGGAGGAGGTGGTTCC  
TGGCGGGGGCCGCAGCAAGAGGGATCCAGATCTCTACCAGCTGCTCCAGAGACTCTTCAAAG  
CCACTCATCTCTGGAGGGATTGCTCAAAGCCCTGAGCCAGGCTAGCACAGATCCTAAGGAATC  
AACATCTCCCGAGAAACGTGACATGCATGACTTCTTTGTGGGACTTATGGGCAAGAGGAGCGT  
CCAGCCAGAGGGAAAGACAGGACCTTTCTTACCTTCAGTGAGGGTTCCCTCGGCCCTTCATCC  
CAATCAGCTTGGATCCACAGGAAAGTCTTCCCTGGGAACAGAGGAGCAGAGACCTTTATAAGA  
CTCTCCTACGGATGTGAATCAAGAGAACGTCCCCAGCTTTGGCATCCTCAAGTATCCCCGAG  
AGCAGAATAGGTACTCCACTTCCGGA CTCTGGACTGCATTAGGAAGACCTCTTCCCTGTCC  
CAATCCCCAGGTGCGCACGCTCCTGTTACCCTTTCTCTTCCCTGTTCTTGTAACATTCTTG  
CTTTGACTCCTTCTCCATCTTTTCTACCTGACCCTGGTGTGGAACTGCATAGTGAATATCCC  
CAACCCCAATGGGCATTGACTGTAGAATAACCTAGAGTTCCTGTAGTGTCTACATTAAAAAT  
ATAATGTCTCTCTATTCTCAACAATAAAGGATTTTGCATATGAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAA

448/615

**FIGURE 444**

MRIMLLFTAILAFSLAQSFQAVCKEPQEEVVPGGGRSKRDPDLYQLLQRLFKSHSSLEGLLKA  
LSQASTDPKESTSPEKRDMDHDFVGLMGKRSVQPEGKTGPFLPSVRVPRPLHPNQLGSTGKSS  
LGTEEQRPL

**Important features:**

**Signal peptide:**

amino acids 1-18

**Tyrosine kinase phosphorylation site.**

amino acids 36-45

**N-myristoylation site.**

amino acids 33-39, 59-65

**Amidation site.**

amino acids 90-94

**Leucine zipper pattern.**

amino acids 43-65

**Tachykinin family signature.**

amino acids 86-92

449/615

**FIGURE 445**

TGGACTTCTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTGGGTCACAT  
CCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAGAGATCATCACTCCCTGCCTTTTA  
CCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCCCTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGA  
TGCGGTGGCATCGCTGCTCATCGTGGGGGCGGTGTTCTGTGCGCACGCCACGCCGCAGCCCCGCCCAAGATGG  
CAAAGTCTACATCAACATGCCAGGCAGGGGCTTGACCCTCCTGCAGCTTGGACCTTTGACTTCTGACCTCTCATC  
CTGGATGGTGTGTGGTGGCACAGGAACCCCGCCCCAACTTTTGGATTGTAATAAAACAATTGAAACACCA



450/615

**FIGURE 446**

MIHLGHILFLLLLPVAAAQTTPGERSSLPAYFPGTSGSCSGCSLSLPLLAGLVAADAVASLLIVGAVFLCARPR  
RSPAQDGKVYINMPGRG

Signal peptide:	Amino acids 1-18
transmembrane domain:	Amino acids 51-70
Glycosaminoglycan attachment site:	Amino acids 40-44
N-myristoylation sites:	Amino acids 34-40;37-43;52-58
Prokaryotic membrane lipoprotein lipid attachment site:	Amino acids 29-40

451/615

**FIGURE 447**

GCCAGGTGTGCAGGCCGCTCCAAGCCCAGCCTGCCCCGCTGCCGCCACCATGACGCTCCTCCC  
CGGCCTCCTGTTTCTGACCTGGCTGCACACATGCCTGGCCCACCATGACCCCTCCCTCAGGGG  
GCACCCCCACAGTCACGGTACCCACACTGCTACTCGGCTGAGGAAGTGGCCCTCGGCCAGGC  
CCCCCACACCTGCTGGCTCGAGGTGCCAAGTGGGGGCAGGCTTTGCCTGTAGCCCTGGTGTC  
CAGCCTGGAGGCAGCAAGCCACAGGGGGAGGCACGAGAGGCCCTCAGCTACGACCCAGTGCCC  
GGTGCTGCGGCCGGAGGAGGTGTTGGAGGCAGACACCCACCAGCGCTCCATCTCACCCCTGGAG  
ATACCGTGTGGACACGGATGAGGACCGCTATCCACAGAAGCTGGCCTTCGCCGAGTGCCTGTG  
CAGAGGCTGTATCGATGCACGGACGGGCCGCGAGACAGCTGCGCTCAACTCCGTGCGGCTGCT  
CCAGAGCCTGCTGGTGCTGCGCCGCCGGCCCTGCTCCCGCGACGGCTCGGGGCTCCCCACACC  
TGGGGCCTTTGCCTTCCACACCGAGTTCATCCACGTCCCCGTCGGCTGCACCTGCGTGCTGCC  
CCGTTCAGTGTTGACCGCCGAGGCCGTGGGGCCCCCTAGACTGGACACGTGTGCTCCCCAGAGGG  
CACCCCTATTTATGTGTATTTATTGTTATTTATATGCCTCCCCAACACTACCCTTGGGGTC  
TGGGCATTCCCCGTGTCTGGAGGACAGCCCCCACTGTTCTCCTCATCTCCAGCCTCAGTAGT  
TGGGGGTAGAAGGAGCTCAGCACCTCTCCAGCCCTTAAAGCTGCAGAAAAGGTGTCACACGG  
CTGCCTGTACCTTGGCTCCCTGTCCTGCTCCCGGCTTCCCTTACCCTATCACTGGCCTCAGGC  
CCCGCAGGCTGCCTCTTCCCAACCTCCTTGGAAGTACCCCTGTTTCTTAAACAATTATTTAAG  
TGACGTGTATTATTAACTGATGAACACATCCCCAAA

452/615

## **FIGURE 448**

MTLLPGLLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPLGQAPPHLLARGAKWGQALP  
VALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPWRYRVDTDEDYPQKLAF  
AECLCRGCIDARTGRETAALNSVRLQLSLLVLRRRPCSRDGSGLPTPGAFAFHTEFIHVPVGC  
TCVLPRSV

**Important features:**

**Signal peptide:**

amino acids 1-18

**Tyrosine kinase phosphorylation site.**

amino acids 112-121

**N-myristoylation sites.**

amino acids 32-38, 55-61, 133-139

**Leucine zipper pattern.**

amino acids 3-25

**Homologous region to IL-17.**

amino acids 99-195

453/615

**FIGURE 449**

TGCAGAGCTTGTGGAGGCC**AT**GGGGCGCGTCGTCGCGGAGCTCGTCTCCTCGCTGCTGGGGTT  
GTGGCTGTTGCTGTGCAGCTGCGGATGCCCGAGGGCGCCGAGCTGCGTGCTCCGCCAGATAA  
AATCGCGATTATTGGAGCCGGAATTGGTGGCACTTCAGCAGCCTATTACCTGCGGCAGAAATT  
TGGGAAAGATGTGAAGATAGACCTGTTTGAAAGAGAAGAGGTCGGGGGGCCGCTGGCTACCAT  
GATGGTGCAGGGGCAAGAATACGAGGCAGGAGGTTCTGTCTATCCATCCTTTAAATCTGCACAT  
GAAACGTTTTGTCAAAGACCTGGGTCTCTCTGCTGTTTCAGGCCCTCTGGTGGCCTACTGGGGAT  
ATATAATGGAGAGACTCTGGTATTTGAGGAGAGCAACTGGTTCATAATTAACGTGATTAAAT  
AGTTTGGCGCTATGGATTTCAATCCCTCCGTATGCACATGTGGGTAGAGGACGTGTTAGACAA  
GTTTCATGAGGATCTACCGCTACCAGTCTCATGACTATGCCTTCAGTAGTGTCGAAAAATTACT  
TCATGCTCTAGGAGGAGATGACTTCCTTGGAATGCTTAATCGAACACTTCTTGAAACCTTGCA  
AAAGGCCGGCTTTTCTGAGAAGTTCCTCAATGAAATGATTGCTCCTGTTATGAGGGTCAATTA  
TGGCCAAAGCACGGACATCAATGCCTTTGTGGGGCGGTGTCACTGTCCTGTTCTGATTCTGG  
CCTTTGGGCAGTAGAAGGTGGCAATAAACTTGTTTGCTCAGGGCTTCTGCAGGCATCCAAAAG  
CAATCTTATATCTGGCTCAGTAATGTACATCGAGGAGAAAACAAAGACCAAGTACACAGGAAA  
TCCAACAAAGATGTATGAAGTGGTCTACCAATTGGAAGTCTGAGACTCGTTCAGACTTCTATGA  
CATCGTCTTGGTGGCCACTCCGTTGAATCGAAAAATGTGCAATATTACTTTTCTCAACTTTGA  
TCCTCCAATTGAGGAATTCCATCAATATTATCAACATATAGTGACAACTTTAGTTAAGGGGGA  
ATTGAATACATCTATCTTTAGCTCTAGACCCATAGATAAATTTGGCCTTAATACAGTTTTAAC  
CACTGATAATTCAGATTTGTTTATTACAGTATTGGGATTGTGCCCTCTGTGAGAGAAAAGGA  
AGATCCTGAGCCATCAACAGATGGAACATATGTTTGGAAGATCTTTTCCCAAGAACTCTTAC  
TAAAGCACAAATTTTAAAGCTCTTTCTGTCCTATGATTATGCTGTGAAGAAGCCATGGCTTGC  
ATATCCTCACTATAAGCCCCCGAGAAATGCCCTCTATCATTCTCCATGATCGACTTTATTA  
CCTCAATGGCATAGAGTGTGCAGCAAGTGCCATGGAGATGAGTGCCATTGCAGCCCACAACGC  
TGCACTCCTTGCCCTATCACCGCTGGAACGGGCACACAGACATGATTGATCAGGATGGCTTATA  
TGAGAACTTAAACTGAAC**TGA**AGTGACACACTCCTTTTTCCCCTCCTAGTTCCAAATGA  
CTATCAGTGGCAAAAAGAACAAATCTGAGCAGAGATGATTTTGAACCAGATATTTTGCCAT  
TATCATTGTTTAATAAAAGTAATCCCTGCTGGTCATAGGAAAAAAAAAAAAA

454/615

**FIGURE 450**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62880
<subunit 1 of 1, 505 aa, 1 stop
<MW: 56640, pI: 6.10, NX(S/T): 4
MGRVVAELVSSLLGLWLLLCSCGCPEGAELRAPDPKIAIIGAGIGGTSAAYYLRQKFGKDVKI
DLFEREEVGGRLATMMVQGOEYEAGGSVIHPLNLHMKRFVKDLGLSAVQASGGLLGIYNGETL
VFEESNWFIIINVIKLVWRYGFQSLRMHMWVEDVLDKFMRIYRYQSHDYAFSSVEKLLHALGGD
DFLGLMLNRTLLETLOKAGFSEKFLNEMIAPVMRVNYGQSTDINAFVGAVSLSCSDSGLWAVEG
GNKLVCSGLLQASKSNLISGSVMYIEEKTCTKYTGNTKMYEVVYQIGTETRSDFYDIVLVAT
PLNRKMSNITFLNFDPPIEEFHQYYQHIVTTLVKGELNTSIFSSRPIDKFGLNTVLTDDNSDL
FINSIGIVPSVREKEDPEPSTDGTYVWKIFSQETLTKAQILKLFLSYDYAVKKPWLAYPHYKP
PEKCPSSIILHDLRYLNGIECAASAMEMSAIAAHNAALLAYHRWNGHTDMIDQDGLYEKLKTEL
```

**Important features:****Signal peptide:**

amino acids 1-23

**N-glycosylation sites.**

amino acids 196-200, 323-327, 353-357

**Tyrosine kinase phosphorylation site.**

amino acids 291-298

**N-myristoylation sites.**amino acids 23-29, 41-47, 43-49, 45-51, 46-52, 72-78, 115-121,  
119-125, 260-266, 384-390, 459-465**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 12-23, 232-243

455/615

**FIGURE 451**

CAACCATGCAAGGACAGGGCAGGAGAAGAGGAACCTGCAAAGACATATTTTGTTCAAAATGG  
CATCTTACCTTTATGGAGTACTCTTTGCTGTTGGCCTCTGTGCTCCAATCTACTGTGTGTCCC  
CGGCCAATGCCCCCAGTGCATACCCCGCCCTTCCTCCACAAAGAGCACCCCTGCCTCACAGG  
TGTATTCCCTCAACACCGACTTTGCCTTCCGCCTATACCGCAGGCTGGTTTTGGAGACCCCGA  
GTCAGAACATCTTCTTCTCCCCTGTGAGTGTCTCCACTTCCCTGGCCATGCTCTCCCTTGGGG  
CCCACTCAGTCACCAAGACCCAGATTCTCCAGGGCCTGGGCTTCAACCTCACACACACACCAG  
AGTCTGCCATCCACCAGGGCTTCCAGCACCTGGTTCACTCACTGACTGTTCCAGCAAAGACC  
TGACCTTGAAGATGGGAAGTGCCTCTTCGTCAAGAAGGAGCTGCAGCTGCAGGCAAATTTCT  
TGGGCAATGTCAAGAGGCTGTATGAAGCAGAAGTCTTTTCTACAGATTTCTCCAAACCCCTCCA  
TTGCCCAGGCGAGGATCAACAGCCATGTGAAAAAGAAGACCCAAGGGAAGGTTGTAGACATAA  
TCCAAGGCCTTGACCTTCTGACGGCCATGGTCTGGTGAATCACATTTTCTTTAAAGCCAAGT  
GGGAGAAGCCCTTTACCTTGAATATACAAGAAAGAACTTCCCATTCCTGGTGGGCGAGCAGG  
TCACTGTGCAAGTCCCCATGATGCACCAGAAAGAGCAGTTTCGCTTTTGGGGTGGATACAGAGC  
TGAAGTCTTTGTGCTGCAGATGGATTACAAGGGAGATGCCGTGGCCTTCTTTGTCTCCCTA  
GCAAGGGCAAGATGAGGCAACTGGAACAGGCCTTGTGAGCCAGAACACTGATAAAGTGGAGCC  
ACTCACTCCAGAAAAGGTGGATAGAGGTGTTTCATCCCCAGATTTTCCATTTCTGCCTCCTACA  
ATCTGGAAACCATCCTCCCGAAGATGGGCATCCAAAATGCCTTTGACAAAAATGCTGATTTTT  
CTGGAATTGCAAAGAGAGACTCCCTGCAGGTTTCTAAAGCAACCCACAAGGCTGTGCTGGATG  
TCAGTGAAGAGGGCACTGAGGCCACAGCAGCTACCACCACCAAGTTCATAGTCCGATCGAAGG  
ATGGTCCCTCTTACTTCACTGTCTCCTTCAATAGGACCTTCCTGATGATGATTACAAATAAAG  
CCACAGACGGTATTCTCTTTCTAGGGAAAGTGGAAAATCCCACTAAATCCTAGGTGGGAAATG  
GCCTGTTAACTGATGGCACATTGCTAATGCACAAGAAATAACAAACCACATCCCTCTTTCTGT  
TCTGAGGGTGCATTTGACCCAGTGGAGCTGGATTGCTGGCAGGGATGCCACTTCCAAGGCT  
CAATCACCAAACCATCAACAGGGACCCAGTCAACAAGCCAACACCCATTAACCCAGTCAGTG  
CCCTTTTCCACAAATTCTCCAGGTAAGTACTAGCTTCATGGGATGTTGCTGGGTTACCATATTC  
CATTCCTTGGGGCTCCAGGAATGGAAATACGCCAACCCAGGTTAGGCACCTCTATTGCAGAA  
TTACAATAACACATTCAATAAACTAAATATGAATTCAAAAAAAAAAAAAAAAAAAAAAAAA  
AA

456/615

**FIGURE 452**

MASYLYGVLFVAVGLCAPIYCVSPANAPSAYPRPSSTKSTPASQVYSLNTDFAFRLYRRLVLET  
PSQNIFFSPVSVSTSLAMLSLGAHSVTKTQILQGLGFNLTHTPESAIHQGFQHLVHSLTVPSK  
DTLKMGSALFVKKELQLQANFLGNVKRLYEAEVFSTDFSNPSIAQARINSHVKKKTQGKVVD  
IIQGLDLLTAMVLVNHIFFKAKWEKPFHLEYTRKNFPFLVGEQVTVQVPMMHQKEQFAFGVDT  
ELNCFVLQMDYKGDVAFFVLPSKGKMRQLEQALSARTLIKWSHSLQKRWIEVFIPRFSISAS  
YNLETILPKMGIQNAFDKNADFSGIAKRDSLQVSKATHKAVLDVSEEGTEATAATTTKFIVRS  
KDGPSYFTVSEFNRTFLMMITNKATDGILFLGKVENPTKS

**Signal peptide:**  
amino acids 1-20

457/615

**FIGURE 453**

CTCCGGGTCCCCAGGGGCTGCCCGGGCCGGCCTGGCAAGGGGGACGAGTCAGTGGACACTCCAGGAAGAGCGGC  
CCCCGGGGGGCGATGACCGTGCGCTGACCCTGACTCACTCCAGGTCCGGAGGCGGGGCCCCGGGGCGACTCG  
GGGGCGGACCGCGGGGCGGAGCTGCCGCCCGTGAGTCCGGCCGAGCCACCTGAGCCCGAGCCGCGGGACACCGTC  
GCTCCTGCTCTCCGAATGCTGCGCACCGCGATGGGCCTGAGGAGCTGGCTCGCCGCCCATGGGGCGCGCTGCCG  
CCTCGGCCACCGCTGCTGCTGCTCCTGCTGCTGCTGCTCCTGCTGCAGCCGCCCTCCGACCTGGGCGCTCAGC  
CCCCGGATCAGCCTGCCTCTGGGCTCTGAAGAGCGGCCATTCTCAGATTGGAAGCTGAACACATCTCCAACCTAC  
AACCTCAGCTTCTGCCAGGCGGGGAGTACCAGGAGCTGCTTTGGGGTGCAGACGCAGAGAAGAAACAGCAGTGC  
AGCTTCAAGGGCAAGGACCCACAGCGCGACTGTCAAACTACATCAAGATCCTCCTGCCGCTCAGCGGCAGTCAC  
CTGTTACCTGTGGCACAGCAGCCTTCAGCCCCATGTGTACCTACATCAACATGGAGAATTCACCCTGGCAAGG  
GACGAGAAGGGGAATGTCTCCTGGAAGATGGCAAGGCGGTTGTCCCTTCGACCCGAATTTCAAGTCCACTGCC  
CTGGTGGTTGATGGCGAGCTCTACACTGGAACAGTCAGCAGCTTCCAAGGGAATGACCCGGCCATCTCGCGGAGC  
CAAAGCCTTCGCCCCACCAAGACCGAGAGCTCCCTCAACTGGCTGCAAGACCCAGCTTTTGTGGCCTCAGCCTAC  
ATTCTGAGAGCCTGGGCGAGCTTGCAGGCGATGATGACAAGATCTACTTTTTCTTCAGCGAGACTGGCCAGGAA  
TTTGAGTTCTTTGAGAACACCATTTGTGTCCGCGATTGCCCGCATCTGCAAGGGCGATGAGGGTGGAGAGCGGGTG  
CTACAGCAGCGCTGGACCTCCTCCTCAAGGCCAGCTGCTGTGCTCACGGCCGACGATGGCTTCCCTTCAAC  
GTGCTGCAGGATGTCTTCAGCTGAGCCCCAGCCCCAGGACTGGCGTGACACCCTTTTCTATGGGTCTTCACT  
TCCAGTGGCACAGGGGAACCTACAGAAGGCTCTGCCGTCTGTGCTTCAATGAAGGATGTGCAGAGAGTCTTC  
AGCGGCCCTTACAAGGAGGTGAACCGTGAGACACAGCAGTGGTACACCGTGACCCACCCGGTGCCACACCCCGG  
CCTGGAGCGTGATCACCAACAGTGCCCGGGAAAGGAAGATCAACTCATCCCTGCAGCTCCCAGACCGCTGCTG  
AATTCTCAAGGACCACTTCTGATGGACGGGAGGTCCGAAGCCGATGCTGCTGCTGCAGCCCCAGGCTCGC  
TACCAGCGGTGGCTGTACACCGCTCCCTGGCCTGCACCACACCTACGATGTCTCTTCTGGGCACTGGTGAC  
GGCCGGCTCCACAAGGCAGTGAGCGTGGGCCCCGGGTGCACATCATTGAGGAGCTGCAGATCTTCTCATCGGGA  
CAGCCCGTGCAGAATCTGCTCCTGGACACCCACAGGGGGTCTGTATGCGGCCCTCACACTCGGGCGTAGTCCAG  
GTGCCCATGGCCAACAGCTGCAGCTGTACCGGAGCTGTGGGACTGCCTCCTCGCCCGGGACCCCTACTGTGCTTG  
AGCGGCTCCAGCTGCAAGCAGCTCAGCCTCTACCAGCCTCAGCTGGCCACCAGGCGGTGGATCCAGGACATCGAG  
GGAGCCAGCGCCAAGGACCTTTCAGCGCGCTTTCGGTTGTGTCCCGCTCTTTTGTACCAACAGGGGAGAAGCCA  
TGTGAGCAAGTCCAGTTCAGCCCCAACAGTGAACACTTTGGCCTGCCCGCTCCTCTCCAACCTGGCGACCCGA  
CTCTGGCTACGCAACGGGGCCCCCTCAATGCCTCGCCTCCTGCCACGTGCTACCCACTGGGGACCTGCTGCTG  
GTGGGCAACCAACAGCTGGGGGAGTTCCAGTGCTGGTCACTAGAGGAGGGCTTCAGCAGCTGGTAGCCAGCTAC  
TGCCAGAGGTGGTGGAGGACGGGGTGGCAGACCAACAGATGAGGGTGGCAGTGTACCCGTCAATTATCAGCACA  
TCGCGTGTGAGTGACACAGCTGGTGGCAAGGCCAGCTGGGGTGCAGACAGGTCTACTGGAAGGAGTTCTGGTG  
ATGTGCACGCTCTTTGTGCTGGCGTGTGCTCCAGTTTTATTCTTGCTCTACCGGCACCGGAACAGCATGAAA  
GTCTTCTGAAGCAGGGGAATGTGCCAGCGTGACCCCAAGACCTGCCCTGTGGTGTGCCCTTGAGACCCGC  
CCACTCAACGGCCTAGGGCCCCCTAGCACCCCGCTCGATACCCGAGGGTACCAGTCCCTGTGAGACAGCCCCCG  
GGGCCCCGAGTCTTCACTGAGTCAGAGAAGAGGCCACTCAGCATCCAAGACAGCTTCGTGGAGGTATCCCCAGTG  
TGCCCCGGCCCCGGGTCCGCTTGGCTCGGAGATCCGTGACTCTGTGGTGTGAGAGCTGACTTCCAGAGGACGC  
TGCCCTGGCTTCAGGGGCTGTGAATGCTCGGAGAGGGTCAACTGGACCTCCCTCCGCTCTGCTCTTCTGGAAC  
ACGACCGTGGTGCCCGGCCCTTGGGAGCCTTGGAGCCAGCTGGCCTGCTGCTCTCAGTCAAGTAGCGAAGCTCC  
TACCACCCAGACACCAACAGCCGTGGCCCCAGAGTCTTGCCCAATATGGGGGCTGCCCTAGGTGGTGGAA  
CAGTGCTCCTTATGTAACTGAGCCCTTTGTTTAAAAAACAAATCCAAATGTGAACTAGAATGAGAGGGAAGAG  
ATAGCATGGCATGCAGCACACCGCTGCTCCAGTTTATGGCCTCCAGGGGTGCTGGGGATGCATCCAAGTGG  
TTGCTGTGAGACAGAGTTGGAAACCTCACCAACTGGCCTCTTACCTTCCACATTATCCGCTGCCACCGGCTGC  
CCTGTCTCACTGCAGATTAGGACAGCTTGGGCTGCGTGCGTTCTGCCCTTGCCAGTCAGCCGAGGATGTAGTTG  
TTGCTGCCGTGCTCCACACCTCAGGGACAGAGGGTAGGTGGCACTGCGGCCCTCACCAGTCTCTGGGCTC  
GGACCAACTCCTGGACCTTTCAGCCTGTATCAGGCTGTGGCCACACGAGAGGACAGCGGAGCTCAGGAGAGA  
TTTCGTGACAATGTACGCCTTTCCTCAGAATTGAGGGAAGAGACTGTGCGCTGCCTTCTCCGTGTTGCGTGA  
GAACCCGTGTGCCCTTCCACCATATCCACCTCGCTCCATCTTGAACCAACACGAGGAAGTAAGTGCACC  
CTGGTCTCTCCCGAGTCCCGAGTTACCCCTCCATCCCTCACCTTCTCCACTCTAAGGGATATCAACACTGCCC  
AGCACAGGGGCCCTGAATTTATGTGGTTTTTATACATTTTTTAATAAGATGCACTTTATGTCATTTTTAATAAA  
GTCTGAAGAATTACTGTTTAAAAA



458/615

**FIGURE 454**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA67962 .
><subunit 1 of 1, 837 aa, 1 stop
><MW: 92750, pI: 7.04, NX(S/T): 6
MLRTAMGLRSWLAAPWGALPPRPPLLLLLLLLLLLLLLQPPPPTWALSPRISLPLGSEERPFLRFE
AEHISNYTALLLSRDGRTLYVGAREALFALSSNLSFLPGGEYQELLWGADAEEKKQQCSFKGKD
PQRDCQNYIKILLPLSGSHLFTCGTAAAFSPMCTYINMENFTLARDEKGNVLLEDGKGRCPFDP
NFKSTALVVDGELYTGTVSSFQGNPAISRSQSLRPTKTESSLNWLQDPAFVASAYIPESLGS
LQGDDDDKIYFFFSETGQEFEEFFENTIVSRIARICKGDEGGERVLQQRWTSFLKAQLLCSRPDD
GFPFNVLQDVFTLSPSPQDWRDTLFGYGVFTSQWHRGTTEGSAVCVFTMKDVQRVFSGLYKEVN
RETQQWYTVTHPVPTPRPGACITNSARERKINSSLQLPDRVLNFLKDHFLMDGQVRSRMLLLQ
POARYQRVAVHRVPGLHHTYDVLFLGTGDGRLHKAVSVGPRVHIIEELQIFSSGQPVQNLLLD
THRGLLYAASHSGVVQVPMANCSLYRSCGDCLLARDPYCAWSGSSCKHVSLEYQPLATRPWIQ
DIEGASAKDLCSASSVVSPSFVPTGEKPCQVQFQPNVTNLTACPLLSNLATRLWLRNGAPVN
ASASCHVLPTGDLVLVGTOQLGEFQCWSLEEGFQQLVASYCPEVVEDGVADQTDGGSPVPII
STSRVSAPAGGKASWGADRSYWKEFLVMCTLFVLAVLLPVLFLLYRHRNSMKVFLKQGECAV
HPKTCPVVLPPETRPLNGLGPPSTPLDHRGYQSLSDSPPGARVFTSEKRPLSIQDSFVEVSP
VCPRPRVRLGSEIRDSVV
```

**Transmembrane domains:**

amino acids 23-46 (type II), 718-738

459/615

**FIGURE 455**

TAAGATGAGGGCATCCCTCACGTTACACCCCTGGTGGCATCTGCCAGCCCTGTTCTGGGGAC  
AAGGCGGGCTTTCGTGGGAGCCATGCTCAGCCTGCCAGGAAGCCAAGCCCTACAGTGCAGAGG  
AAACAGAATTTCAACGGGAAGCTGGTTTGCTTCATACCATTGGGATCTGCTGGTAAAGCTGTT  
ATTTGGGTTTAGGGACTGATCCCTTGACGTTTACTTCTGGATCACCATGAATGGCCAAGATGG  
TGGCAGAACACGCTGTGGACCCTGAGTTAGAGACAATGCAAATGTTGGATTGGGTGTAATTCT  
TTTTGAATCCCAGATCCAGTCTGTACTTGAATATGAGCAGAAGATCTACAAGAATGCTGACAG  
GGAACCGTGTAAAGACCCAGCACCCCTATTCCCAGGAGCTTCTGGCCTGACCATCTGCAGCCA  
AAGCACTAACAGGGACAGATATGGGAATGTCCACCTTTGATCCGCATCCTGCACAATAGTGGT  
CCCACCATGGCTGCCACTTTTTTATACTATTTGGAGAAAAGACCTTGTATAAATTCGAGGCCC  
GAGTGACTAACGTCTCTGTACACCGGAAATGGGTACTTGGTGGCATAGAGAAACACAATTAGC  
CACTTTTTTACGCTACACTTCTCACTCAGCTGCACCCTACACTTCTCACTCAGGTGCACCCCT  
TCTGCTGTCTTTCCCCAACGTACTGGGTCCCGAGCGTGGTGGGTATTTGCCACACTGGGTGC  
CAGCTCAGCAGCCCCCACCTCTCTTTATTCTCTCCAAAGCTGGTCTTTCTGACTATCATTGT  
GGTAGGGGGAGGACAGATGCTAAAGGTGGAAGCTGACCTGGAGAAAGAGACACACGGGGTGAC  
TGTGGCAAAGGACAGCTGGAAAAGAACTCTATCACTTCTTCATTGGCAACCACAAGGCACCC  
GAGGCCATGGCACTCCCAGAGGCTGTGCGCAGAGCCAAGCCTCTCAACCTCTTCTGGCCCTGC  
GTCCTGCAGCGAAGTCTCTGCTGTAAGACAGTAGACTCCTTCGATGAGGTGCTCAAAAATGCT  
ACCCGGGGTGGTGGTGTCTGGCTTGAGTCTGGCCAGTTGAGAGAAAGTTGCAGAGATCAGGG  
GCCAAGGATGTCATAGCCCCAGGTTGTCTCAGGGTCCCAATCCTAGGGCAGGGTGTGCATGG  
AAGCAAGAACTATGGAAACCTAGCTCCAGTCTGCAGGCTCTGAGCCCCTAGTTCCCTCACTCCA  
GCGGGGCTCCCTCACTGCACAGAACCCACCCCTTCTGTGTGGGCACTGCTGACCACACAGATG  
ACCCAGACCCAAAGAGCCTGGCAGAAGCTCTGTGGTTGGAGCTGGGCTCCGTCTCCAGGTCTG  
GTTGAGGGGGATCAGGAAGGCTCTTTTCCACCTGTGGCTTCACTGGCCCTTTGAGATTTCTTA  
TCTCACCGTTACTTCAATTACCCTTGACAGGGGGCCAGGGAGTCAAGAATATACCGTGTTCCTC  
CAGGGTTTAAAGCCGGCCATGCCTTCCCCGAGAGCATAACCAACTTGACAGGGGTGCCAGTTAC  
CCCACAACTGAAGGAAGGAGATCCTTCCCCCGTCCCCAGGAGTGCTCTCAACCAGCCTCAGA  
AAGCTTGAGAAGATGGACCCCTTGCCCCACCAGGGTTAATTCCTGGTGGGGCAGCTCGGCTGTG  
ATCAGGGCAACCAACCTATAGGAAGCCTTCCAGTGTGAGCTGGAATTAGACTGAACATGTGC  
TTGGGCCTGCCTCTCCCTAGACGCAGTTGCGGGGCACTCCAGGGAATGAACCAGCTCAAGTGT  
GTCCCTAACAGCAGCCTGGAGCTACCCCCAATCCCTCACAGCCTGACCCTCCTCATTCATCA  
GATCTCGTGCCG

460/615

**FIGURE 456**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA69555  
><subunit 1 of 1, 148 aa, 1 stop  
><MW: 16214, pI: 10.22, NX(S/T): 0

MGTWWHRETQLATFSATLLTQLHPTLLTQVHPLLLSFPQRTGSRAWVVFATLGASSAAPH  
LSLFSPKLVFLTIIVVGGGQMLKVEADLEKETHGVTVAKDSWKRNSITSSLATTRHPRPW  
HSQRLCAEPSLSTSSGPASCSEVSAVRQ

**Important features of the protein:****Signal peptide:**

Amino acids 1-28

**Transmembrane domain:**

Amino acids 64-78

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 103-107

**N-myristoylation sites:**

Amino acids 53-59;94-100

461/615

**FIGURE 457**

CCCGCGCGCCCTGGCACTCAATCCCCGCCATGTGGGGGCTCCTGCTCGCCCTGGCCGCCTTC  
GCGCCGGCCGTCGGCCCGGCTCTGGGGGCGCCCAGGAACTCGGTGCTGGGCCTCGCGCAGCCC  
GGGACCACCAAGGTCCCAGGCTCGACCCCGGCCCTGCATAGCAGCCGGCACAGCCGCCGGCG  
GAGACAGCTAACGGGACCTCAGAACAGCATGTCCGGATTTCGAGTCATCAAGAAGAAAAAGGTC  
ATTATGAAGAAGCGGAAGAAGCTAACTCTAACTCGCCCCACCCCACTGGTGACTGCCGGGCC  
CTTGTAACCCCACTCCAGCAGGGACCCTCGACCCCGCTGAGAAACAAGAAACAGGCTGTCCT  
CCTTTGGGTCTGGAGTCCCTGCGAGTTTCAGATAGCCGGCTTGAGGCATCCAGCAGCCAGTCC  
TTTGGTCTTGAGACCACACCGAGGACGGCTCAACATTCATTTCAGGCCTGGAGGACGGCGATCTA  
TATGATGGAGCCTGGTGTGCTGAGGAGCAGGACGCCGATCCATGTTTCAGGTGGACGCTGGG  
CACCCACCCGCTTCTCGGGTGTTATCACACAGGGCAGGAACCTCTGTCTGGAGGTATGACTGG  
GTCACATCATACAAGGTCCAGTTCAGCAATGACAGTCGGACCTGGTGGGGAAGTAGGAACCAC  
AGCAGTGGGATGGACGCAGTATTTCTGCCAATTCAGACCCAGAACTCCAGTGCTGAACCTC  
CTGCCGGAGCCCCAGGTGGCCCGCTTCATTCGCCTGCTGCCCCAGACCTGGCTCCAGGGAGGC  
GCGCCTTGCTCCGGGCAGAGATCCTGGCCTGCCAGTCTCAGACCCCAATGACCTATTCTT  
GAGGCCCTGCGTCGGGATCCTCTGACCTCTAGACTTTTCAGCATCACAATTACAAGGCCATG  
AGGAAGCTGATGAAGCAGGTACAAGAGCAATGCCCCAACATCACCCGCATCTACAGCATTGGG  
AAGAGCTACCAGGGCCTGAAGCTGTATGTGATGGAAATGTCGGACAAGCCTGGGGAGCATGAG  
CTGGGGGAGCCTGAGGTGCGCTACGTGGCTGGCATGCATGGGAACGAGGCCCTGGGGCGGGAG  
TTGCTTCTGCTCCTGATGCAGTTCCTGTGCCATGAGTTCCTGCGAGGGAACCCACGGGTGACC  
CGGCTGCTCTCTGAGATGCGCATTACCTGCTGCCCTCCATGAACCTGATGGCTATGAGATC  
GCCTACCACCGGGGTTTCAGAGCTGGTGGGCTGGGCCGAGGGCCGCTGGAACAACCAGAGCATC  
GATCTTAACCATAATTTTGCTGACCTCAACACACCACTGTGGGAAGCACAGGACGATGGGAAG  
GTGCCCCACATCGTCCCCAACCATCACCTGCCATTGCCCACTTACTACACCTGCCCAATGCC  
ACCGTGGCTCCTGAAACGCGGGCAGTAATCAAGTGGATGAAGCGGATCCCCTTTGTGCTAAGT  
GCCAACCTCCACGGGGGTGAGCTCGTGGTGTCTTACCCATTCGACATGACTCGCACCCCGTGG  
GCTGCCCGCGAGCTCACGCCACACCAGATGATGCTGTGTTTCGCTGGCTCAGCACTGTCTAT  
GCTGGCAGTAATCTGGCCATGCAGGACACCAGCCGCCGACCCTGCCACAGCCAGGACTTCTCC  
GTGCACGGCAACATCATCAACGGGGCTGACTGGCACACGGTCCCCGGGAGCATGAATGACTTC  
AGCTACCTACACACCAACTGCTTTGAGGTCACTGTGGAGCTGTCTGTGACAAGTTCCCTCAC  
GAGAATGAATTGCCCCAGGAGTGGGAGAACAACAAGACGCCCTCCTCACCTACCTGGAGCAG  
GTGCGCATGGGCATTGCAGGAGTGGTGAGGGACAAGGACACGGAGCTTGGGATTGCTGACGCT  
GTCATTGCCGTGGATGGGATTAACCATGACGTGACCACGGCGTGGGGCGGGGATTATTGGCGT  
CTGCTGACCCCAAGGGGACTACATGGTGACTGCCAGTGCCGAGGGCTACCATTTCAGTGACACGG  
AACTGTCGGGTACCTTTGAAGAGGGCCCCCTTCCCCTGCAATTTTCGTGCTACCAAGACTCCC  
AAACAGAGGCTGCGCGAGCTGCTGGCAGCTGGGGCCAAGGTGCCCCCGGACCTTCGCAGGCGC  
CTGGAGCGGCTAAGGGGACAGAAGGATTGATACCTGCGGTTTAAGAGCCCTAGGGCAGGCTGG  
ACCTGTCAAGACGGGAAGGGGAAGAGTAGAGAGGGAGGGACAAAGTGAGGAAAAGGTGCTCAT  
TAAAGCTACCGGGCACCTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

462/615

**FIGURE 458**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71162
><subunit 1 of 1, 734 aa, 1 stop
><MW: 81677, pI: 6.60; NX(S/T): 6
MWGLLLALAAFAVAVGPAVGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS
EQHVRIRVIKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTPAGTLDPAEKQETGCPPLGL
ESLRVSDSRLEASSSQSFGLGPHRGRLNIHSGLEDGDLYDGAWCAEEQDADPWFQVDAGH
PTRFSGVITQGRNSVWRYDWVTSYKVQFSNDSRTWWGSRNHSSGMDAVFPANSDPETPVL
NLLPEPQVARFIRLLPQTWLQGGAPCLRAEILACPVSDPNDLFLEAPASGSSDPLDFQHH
NYKAMRKLKQVQECPNITRIYSIGKSYQGLKLYVMEMSDKPGEHELGEPEVRYVAGMH
GNEALGRELLLLLLMQFLCHEFLRGNPRVTRLLSEMRIHLLPSMNPDGYEIAHYHRSSELVG
WAEGRWNNQSIDLNHNFADLNTPLWEAQDDGKVPHVPHVNHHLPLPTYYTLPNATVAPETR
AVIKWMKRIPFVLSANLHGGEVVSYPFDMTRTPWAARELTPTPDDAVFRWLSTVYAGSN
LAMQDTSRRPCHSQDFSVHGNIINGADWHTVPGSMNDFSYLHTNCFEVTVELSCDKFPHE
NELPQEWENNKDALLTYLEQVRMGIAGVVRDKDTELGIADAVIAVDGINHDVTTAWGGDY
WRLLTGDMVTASAEGYHSVTRNCRVTFEEGPFPCNFVLTKTPKQRLRELLAAGAKVPP
DLRRRLERLRGQKD
```

463/615

**FIGURE 459**

TAAACAGCTACAATATTCCAGGGCCAGTCACTTGCCATTTCTCATAACAGCGTCAGAGAGAA  
AGAACTGACTGAAACGTTTGAGATGAAAGAAAGTTCTCCTCCTGATCACAGCCATCTTGGCAGT  
GGCTGTTGGTTTCCCAGTCTCTCAAGACCAGGAACGAGAAAAAGAAGTATCAGTGACAGCGA  
TGAATTAGCTTCAGGGTTTTTTGTGTTCCCTTACCCATATCCATTTGCCCCACTTCCACCAAT  
TCCATTTCCAAGATTTCCATGGTTTAGACGTAATTTTCCTATTCCAATACCTGAATCTGCCCC  
TACAACTCCCCTTCCTAGCGAAAAGTAAACAAGAAGGATAAGTCACGATAAACCTGGTCACCT  
GAAATTGAAATTGAGCCACTTCCTTGAAGAATCAAAATTCCTGTTAATAAAAGAAAAACAAAT  
GTAATTGAAATAGCACACAGCATTCTCTAGTCAATATCTTTAGTGATCTTCTTTAATAAACAT  
GAAAGCAAAGATTTTGGTTTCTTAATTTCCACA

464/615

**FIGURE 460**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71290 .  
><subunit 1 of 1, 85 aa, 1 stop  
><MW: 9700, pI: 9.55, NX(S/T): 0  
MKKVLLLLITAILAVAVGFPVSQDQEREKRSISDSDELASGFFVFPYPYFPRPLPPIPFPRFPW  
FRNFPPIPIPIESAPTTPLPSEK

**Important features of the protein:****Signal peptide:**

amino acids 1-17

**Homologous region to B3-hordein:**

amino acids 47-85

**Important features of the protein:****Signal peptide:**

Amino acids 1-20

**N-glycosylation sites:**

Amino acids 57-61;210-214;220-224;318-322;428-432;472-476

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 80-84

**N-myristoylation sites:**Amino acids 3-9;20-29;39-48;152-161;161-170;262-271;358-364;  
538-544;560-566;637-643**Zinc carboxypeptidases, zinc-binding region 2 signature:**

Amino acids 498-509

**Zinc carboxypeptidases:**

Amino acids 391-411

465/615

**FIGURE 461**

AGCAGGAGCAGGAGAGGGACAATGGAAAGCTGCCCCGTCCAGGTTGATGTTCTTCTTATTTCTC  
CTCACGTGTGAGCTGGCTGCAGAAGTTGCTGCAGAAGTTGAGAAATCCTCAGATGGTCTGGT  
GCTGCCAGGAACCCACGTGGCTCACAGATGTCCAGCTGCCATGGAATTCATTGCTGCCACT  
GAGGTGGCTGTCATAGGCTTCTTCCAGGATTTAGAAATACCAGCAGTGCCATACTCCATAGC  
ATGGTGCAAAAATTCCCAGGCGTGTCAATTTGGGATCAGCACTGATTCTGAGGTTCTGACACAC  
TACAACATCACTGGGAACACCATCTGCCTCTTTCGCCTGGTAGACAATGAACAACTGAATTTA  
GAGGACGAAGACATTGAAAGCATTGATGCCACCAAATTGAGCCGTTTCATTGAGATCAACAGC  
CTCCACATGGTGACAGAGTACAACCCTGTGACTGTGATTGGGTTATTCAACAGCGTAATTCAG  
ATTCATCTCCTCCTGATAATGAACAAGGCCTCCCCAGAGTATGAAGAGAACATGCACAGATAC  
CAGAAGGCAGCCAAGCTCTTCCAGGGGAAGATTCTCTTTATTCTGGTGGACAGTGGTATGAAA  
GAAAATGGGAAGGTGATATCATTTTTTCAAATAAAGGAGTCTCAACTGCCAGCTTTGGCAATT  
TACCAGACTCTAGATGACGAGTGGGATACACTGCCCACAGCAGAAGTTTCCGTAGAGCATGTG  
CAAACTTTTGTGATGGATTCTTAAGTGGAAAATTGTTGAAAGAAAATCGTGAATCAGAAGGA  
AAGACTCCAAAGGTGGAACCTTGACTTCTCCTTGGAACACATATGGCCAAGTATCTACTTTA  
TGCAAAGTAAAAAGGCACAACCTCAAATCTCAGAGACACTAAACAACAGGATCACTAGGCCTGC  
CAACCACACACACACGCACGTGCACACACGCACGCACGCGTGACACACACACGCGCACACAC  
ACACACACACAGAGCTTCATTTCTGTCTTAAATCTCGTTTTCTCTTCTTCTTCTTTTAAA  
TTTCATATCCTCACTCCCTATCCAATTTCTTCTTATCGTGCATTCTACTCTGTAAGCCCAT  
CTGTAACACACCTAGATCAAGGCTTTAAGAGACTCACTGTGATGCCTCTATGAAAGAGAGGCA  
TTCCTAGAGAAAGATTGTTCCAATTTGTCAATTTAATATCAAGTTTGTATACTGCACATGACTT  
ACACACAACATAGTTCTGCTCTTTTAAAGGTTACCTAAGGGTTGAAACTCTACCTTCTTTTCA  
AAGCACATGTCCGTCTCTGACTCAGGATCAAAAACCAAAGGATGGTTTTAAACACCTTTGTGA  
AATTGTCTTTTTTGCCAGAAGTTAAAGGCTGTCTCCAAGTCCCTGAACTCAGCAGAAATAGACC  
ATGTGAAAACCTCCATGCTTGGTTAGCATCTCCAACCTCCCTATGTAAATCAACAACCTGCATAA  
TAAATAAAAGGCAATCATGTTATA



466/615

**FIGURE 462**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76401
><subunit 1 of 1, 273 aa, 1 stop
><MW: 30480, pI: 4.60, NX(S/T): 1
MEAAPSRFMFLFLLTCELAEEVAAEVEKSSDGPAAQEPTWLTDVPAAMEFIAATEVAVIGF
FQDLEIPAVPILHSMVQKFPGVSFGISTDSEVLTHYNITGNTICLFRVDNEQLNLEDEDIES
IDATKLSRFIEINSLHMTVEYNPVTVIGLFNSVIQIHLLIMNKASPEYEENMHRYQKAALF
QGKILFILVDSGMKENGKVISFFKLKESQLPALAIYQTLDDDEWDTLPTAEVSVEHVQNFCDF
LSGKLLKENRESEGKTPKVEL
```

**Signal peptide:**  
amino acids 1-20

**Transmembrane domain:**  
amino acids 143-162

467/615

**FIGURE 463**

CTCGCTTCTTCCTTCTGGATGGGGGCCCAGGGGGCCCAGGAGAGTATAAAGGCGATGTGGAGG  
GTGCCCCGGCACAACCAGACGCCCAGTCACAGGCGAGAGCCCTGGGATGCACCGGCCAGAGGCC  
ATGCTGCTGCTGCTCAGCTTGCCCTCCTGGGGGGCCCCACCTGGGCAGGGAAGATGTATGGC  
CCTGGAGGAGGCAAGTATTTAGCACCCTGAAGACTACGACCATGAAATCACAGGGCTGCGG  
GTGTCTGTAGGTCTTCTCCTGGTGAAAAGTGTCCAGGTGAACTTGGAGACTCCTGGGACGTG  
AAACTGGGAGCCTTAGGTGGGAATACCCAGGAAGTCACCCTGCAGCCAGGCGAATACATCACA  
AAAGTCTTTGTCGCCTTCCAAGCTTTCCCTCCGGGGTATGGTCATGTACACCAGCAAGGACCGC  
TATTTCTATTTTGGGAAGCTTGATGGCCAGATCTCCTCTGCCTACCCAGCCAAGAGGGGCAG  
GTGCTGGTGGGCATCTATGGCCAGTATCAACTCCTTGGCATCAAGAGCATTGGCTTTGAATGG  
AATTATCCACTAGAGGAGCCGACCACTGAGCCACCAGTTAATCTCACATACTCAGCAAACCTCA  
CCCGTGGGTGCGCTAGGGTGGGGTATGGGGCCATCCGAGCTGAGGCCATCTGTGTGGTGGTGGC  
TGATGGTACTGGAGTAACTGAGTCGGGACGCTGAATCTGAATCCACCAATAAATAAAGCTTCT  
GCAGAAAA

468/615

**FIGURE 464**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76541
><subunit 1 of 1, 178 aa, 1 stop
><MW: 19600, pI: 5.89, NX(S/T): 1
MHRPEAMLLLLTLALLGGPTWAGKMYGPGGGKYFSTTEDYDHEITGLRVSVGLLLVKSQVKL
GDSWDVKLGALGGNTQEVTLQPGYITKVFVAFQAFRLGMVMTSKDRYFYFGKLDGQISSAY
PSQEGQVLVGIYGQYQLLGIKSIGFEWNYPLEEPTTEPPVNLTYSANSPVGR
```

**Signal peptide:**  
amino acids 1-22

469/615

**FIGURE 465**

CGGACGCGTGGGTCCGGCGGCCTGAGGCTGCACCGGGCACGGGTCCGGCCGAATCCAGCCTGGGCGGAGCCGGAG  
TTGCGAGCCGCTGCCTAGAGGCCGAGGAGCTCACAGCTATGGGCTGGAGGCCCGGAGAGCTCGGGGGACCCCGT  
TGCTGCTGCTGCTACTACTGCTGCTGCTCTGGCCAGTGCCAGGCGCCGGGTGCTTCAAGGACATATCCCTGGGC  
AGCCAGTCACCCCGCACTGGGTCTGGATGGACAACCTGGCGCACCGTCAGCCTGGAGGAGCCGGTCTCGAAGC  
CAGACATGGGGTGGTGGCCCTGGAGGCTGAAGGCCAGGAGCTCTGCTTGAGCTGGAGAAGAACCACAGGCTGC  
TGGCCCCAGGATACATAGAAACCCACTACGGCCCCAGATGGGCAGCCAGTGGTGCTGGCCCCCAACCACACGGATC  
ATTGCCACTACCAAGGGCGAGTAAGGGGCTTCCCCGACTCCTGGGTAGTCTCTGCACCTGCTCTGGGATGAGTG  
GCCTGATCACCTCAGCAGGAATGCCAGCTATTATCTGCGTCCCTGGCCACCCCGGGGCTCCAAGGACTTCTCAA  
CCCACGAGATCTTTCGGATGGAGCAGCTGCTCACCTGGAAAGGAACCTGTGGCCACAGGGATCCTGGGAACAAAG  
CGGGCATGACCAGCCTTCTGTGGTGGTCCCCAGAGCAGGGGCGAGCGAGAAGCGCGCAGGACCCGGAAGTACCTGG  
AACTGTACATTGTGGCAGACCACACCTGTTCTTGACTCGGCACCGAACTTGAACCACACCAAAACAGCGTCTCC  
TGGAAGTCGCCAACTACGTGGACAGCTTCTCAGGACTCTGGACATTCAAGGTGGCGCTGACCGGCTGGAGGTG  
GGACCGAGCGGGACCGCAGCCGCTCACGCAGGACGCCAACGCCACGCTCTGGGCTTCTGCACTGGCGCCGGG  
GGCTGTGGGCGCAGCGGCCCCAGACTCCGCGCAGCTGCTCACGGGCGCGCCTTCCAGGGCGCCACAGTGGGCC  
TGGCGCCCGTCGAGGGCATGTGCCGCGCGAGAGCTCGGGAGGCGTGAGCACGGACCACTCGGAGCTCCCCATCG  
CGCCCGCAGCCACCATGGCCCATGAGATCGGCCACAGCCTCGGCTCAGCCACGACCCCGACGGCTGCTGCGTGG  
AGGTGTCGGCGAGTCCGGAGGCTGCGTCATGGCTGCGGCCACCGGGCACCCGTTTCCGCGCGTGTTACAGCGCT  
GCAGCCGCGCCAGCTGCGCGCTTCTTCCGCAAGGGGGCGGCGCTTGCCTCTCCAATGCCCGGACCCCGGAC  
TCCCGGTGCCGCGCGCTCTGCGGGAACGGCTTCTGGAAGCGGGCGAGGAGTGTGACTGCGGCGCTGGCCAGG  
AGTGCCGCGACCTCTGCTGCTTGTCTCACAAGTCTGCTGCGCCCGGGGGCCAGTGCGCCACGGGGACTGCT  
GCGTGCGCTGCTGCTGAAGCCGGCTGGAGCGCTGTGCCGCCAGGCCATGGGTGACTGTGACCTCCCTGAGTTTT  
GCAGGGGACCTCCTCCCACTGTCCCCAGACGTTTACCTACTGGACGGCTCACCTGTGCCAGGGGAGTGGCT  
ACTGCTGGGATGGCGCATGTCCCACGCTGGAGCAGCAGTGCAGCAGCTCTGGGGGCTGGCTCCCACCACTC  
CCGAGGCTGTTTTCCAGGTGGTGAAGTCTGCGGGAGATGCTCATGGAACTGCGGCCAGGACAGCGAGGGCCACT  
TCCTGCCCTGTGCAGGGAGGATGCCCTGTGTGGGAAGTGCAGTGCCAGGGTGGAAAGCCCAGCCTGCTCGCAC  
CGCACATGGTGCCAGTGGACTCTACCGTTACCTAGATGCCAGGAAGTGAAGTGTGCGGGAGCCTTGGCACTCC  
CCAGTGCCAGCTGGACCTGCTTGGCCTGGGCTGGTAGAGCCAGGCACCCAGTGTGGACCTAGAATGGTGTGCC  
AGAGCAGGCGCTGCAGGAAGAATGCCTTCCAGGAGCTCAGCGCTGCCTGACTGCCTGCCACAGCCACGGGGTTT  
GCAATAGCAACCATAACTGCCACTGTGCTCCAGGCTGGGCTCCACCCTTCTGTGACAAGCCAGGCTTTGGTGGCA  
GCATGGACAGTGGCCCTGTGCAGGCTGAAAACCATGACACCTTCTGCTGGCCATGCTCCTCAGCGTCTGCTGC  
CTCTGCTCCAGGGGCGGCGCTGGCCTGGTGTGTGCTACCGACTCCAGGAGCCATCTGCAGCGATGCAGTGGG  
GCTGCAGAAGGGACCCCTGCGTGCAGTGGCCCCAAAGATGGCCCCACAGGGACCAACCCCTGGGCGGCGTTTACC  
CCATGGAGTTGGGCCCCACAGCCACTGGACAGCCCTGGCCCTGGACCCTGAGAACTCTCATGAGCCAGCAGCC  
ACCCTGAGAAGCCTCTGCAGCAGTCTCGCCTGACCCCCAAGCAGATCAAGTCCAGATGCCAAGATCCTGCCTCT  
GGTGAAGAGGTAGCTCCTAAATGAACAGATTTAAAGACAGGTGGCCACTGACAGCCACTCCAGGAACCTTGAAGT  
CAGGGGAGAGCCAGTGAATCACCGACCTCCAGCACCTGCAGGCAGCTTGAAGTTTCTTCCCCGAGTGGAGCT  
TCGACCCACCCACTCCAGGAACCCAGAGCCACATTAGAAGTTCTGAGGGCTGGAGAACACTGCTTGGGCACACT  
CTCCAGCTCAATAAACCATCAGTCCCAGAAGCAAAGGTACACAGCCCTGACCTCCCTCACCAGTGGAGGCTGG  
GTAGTGTGGCCATCCCAAAGGGCTCTGCTCCTGGGAGTCTGGTGTGTCTCTACATGCAATTTCCACGGACCA  
GCTCTGTGGAGGCGATGACTGCTGGCCAGAAGCTAGTGGTCTGGGGCCCTATGGTTGACTGAGTCCACACTCC  
CCTGCAGCCTGGCTGGCCTCTGCAACAAACATAATTTTGGGGACCTTCCCTCTGTTTCTTCCACCCCTGTCTT  
CTCCCTAGGTGGTTCTGAGCCCCACCCCAATCCAGTGTCTACACCTGAGGTTCTGGAGCTCAGAACTGAC  
AGCCTCTCCCCATTCTGTGTGTGTCCGGGGGACAGAGGGAACCATTTAAGAAAAGATACCAAGTAGAAGTCAA  
AAGAAAGACATGTTGGCTATAGGCGTGGTGGCTCATGCCTATAATCCAGCACTTTGGGAAGCCGGGTAGGAGG  
ATCACCAGAGGCCAGCAGGTCCACACCAGCCTGGGCAACACAGCAAGACACCGCATCTACAGAAAAATTTAAAA  
TTAGCTGGGCGTGGTGGTGTGTACCTGTAGGCTAGCTGCTCAGGAGGCTGAAGCAGGAGGATCACTTGAGCCTG  
AGTTCAACACTGCAGTGAAGTATGGTGGCACCCTGCACTCCAGCCTGGGTGACAGAGCAAGACCCTGTCTCTAA  
AATAAATTTTAAAGGACTTAAAAAAGGAAAAAAGAAAAAAGAAAAA

470/615

**FIGURE 466**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76788  
><subunit 1 of 1, 813 aa, 1 stop  
><MW: 87739, pI: 6.94, NX(S/T): 5

MGWRPRRARGTPLLILLILLLLWVPVPGAGVLQGHIPGQPVTPHWVLDGQPWRTVSLEEPVSKPDMGLVALEAEGQ  
ELLLELEKHNHRLAPGYIETHYGPDGQPVVLAPNHTDHCHYQGRVRGFPDSWVVLCTCSGMSGELITLSRNASYYL  
RPWPPRGSKDFSTHEIFRMEQLLTWKGTGHRDPGNKAGMTSLPGGPQSRGRREARRTRKYLELYIVADHTLFLT  
RHRNLNHTKQRLLEVANYVDQLLRTLDIQVALTGLEVWTERDRSRVTQDANATLWAFLOWRRGLWAQRPHDSAQL  
LTGRAFGQATVGLAPVEGMCRAESSGGVSTDHSELPIGAAATMAHEIGHSLGLSHDPDGCCVEAAAESGGCVMAA  
ATGHPFPRVFSACSRRLRAFFRKGGGACLSNAPDPGLPVPPALCGNGFVEAGEECDGPGQECRDLCCFAHNCS  
LRPGAQCAHGDCCVRCCLKPAGALCRQAMGDCDLPEFCTGTSSHCPPDVYLLDGSPCARGSGYCWGDGACPTLEQQ  
CQQLWGP GSHPAPEACFQV VNSAGDAHGNCQDSEGHFLPCAGRDALCGKLQCQGGKPSLLAPHMVPVDSTVHLD  
GQEVTCRGALALPSAQLDLLGLGLVEPGTQCGERMVCQSRRRCRKNAFQELQRCLTACHSHGVCNSNHNCHCAPGW  
APFFCDKPGFGGSMDSGPVQAENHDTFLLAMLLSVLLPLLPGAGLAWCCYRLPGAHLQRCSWGCRDRDPACSGPKD  
GPHRDHPLGGVHPMELGPTATGQPWPLDPENSHEPSSHPEKPLPAVSPDPQADQVQMPSRCLW

**Important features of the protein:****Signal peptide:**

Amino acids 1-27

**Transmembrane domain:**

Amino acids 702-720

**N-glycosylation sites:**

Amino acids 109-113;145-149;231-235;276-280;448-452

**Tyrosine kinase phosphorylation site:**

Amino acids 236-244

**N-myristoylation sites:**

Amino acids 29-35;185-191;195-201;308-314;318-324;326-332;338-344;370-376;  
400-406;402-408;454-460;504-510;510-516;517-523;580-586;  
601-607;661-667;687-693;717-723;719-725

**Amidation site:**

Amino acids 200-204

**Neutral zinc metallopeptidases, zinc-binding region signature:**

Amino acids 342-352

**FIGURE 467**

[illegible]

472/615

**FIGURE 468**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77623  
><subunit 1 of 1, 97 aa, 1 stop  
><MW: 10160, pI: 6.56, NX(S/T): 0  
MQLGTGLLLAAVLSLQLAAAEAIWCHQCTGFGGCSHGSRCLRDSTHCVTTATRVLSNTEDLPL  
VTKMCHIGCPDIPSLGLGPYVSIACCQTSLCNHD

**Important features of the protein:**

**Signal peptide:**

amino acids 1-20

**N-myristoylation sites.**

amino acids 6-11 and 33-38

**Prokaryotic membrane lipoprotein lipid attachment sites.**

amino acids 24-34 and 78-88

473/615

**FIGURE 469**

**C****ATGG****GAGCCTCTTGCAGCTTACCCGCTAAAATGTTCCGGGGCCCAGAGCAAAGGTATTTGCAGT**  
TTTGCTGTCTATAGTTCTATGCACAGTAACGCTATTTCTTCTACAACATAAAATTCCTCAAACC  
TAAAATCAACAGCTTTTATGCCTTTGAAGTGAAGGATGCAAAAGGAAGAACTGTTTCTCTGGA  
AAAGTATAAAGGCAAAGTTTCACTAGTTGTAAACGTGGCCAGTGACTGCCAACTCACAGACAG  
AAATTACTTAGGGCTGAAGGAACTGCACAAAGAGTTTGGACCATCCCACCTCAGCGTGTTGGC  
TTTTCCCTGCAATCAGTTTGGAGAATCGGAGCCCCGCCCAAGCAAGGAAGTAGAATCTTTTGC  
AAGAAAAAACTACGGAGTAACTTTCCCCATCTTCCACAAGATTAAGATTCTAGGATCTGAAGG  
AGAACCTGCATTTAGATTTCTTGTTGATTCTTCAAAGAAGGAACCAAGGTGGAATTTTTGGAA  
GTATCTTGTCAACCCTGAGGGTCAAGTTGTGAAGTTCTGGAGGCCAGAGGAGCCCATTTGAAGT  
CATCAGGCCTGACATAGCAGCTCTGGTTAGACAAGTGATCATAAAAAAGAAAGAGGATCTAT**G**  
**A****GAATGCCATTGCGTTTCTAATAGAACAGAGAAATGTCTCCATGAGGGTTTGGTCTCATT****TTA**  
AACATTTTTTTTTTGGAGACAGTGTCTCACTCTGTCACCCAGGCTGGAGTGCAGTAGTGCGTT  
CTCAGCTCATTGCAACCTCTGCCTTTTTAAACATGCTATTAAATGTGGCAATGAAGGATTTTT  
TTTTAATGTTATCTTGCTATTAAGTGGTAATGAATGTTCCCAGGATGAGGATGTTACCCAAAG  
CAAAAATCAAGAGTAGCCAAAGAATCAACATGAAATATATTAATACTACTTCCTCTGACCATACT  
AAAGAATTCAGAATACACAGTGACCAATGTGCCTCAATATCTTATTGTTCAACTTGACATTTT  
CTAGGACTGTACTTGATGAAAATGCCAACACACTAGACCACTCTTTGGATTCAAGAGCACTGT  
GTATGACTGAAATTTCTGGAATAACTGTAAATGGTTATGTTAATGGAATAAAACACAAATGTT  
GAAAAATGTAAATATATATACATAGATTCAAATCCTTATATATGTATGCTTGTTTTGTGTAC  
AGGATTTTGTTTTTTCTTTTTAAGTACAGGTTCCTAGTGTTTTACTATAACTGTCACTATGTA  
TGTAAGTACATATATAAATAGTCATTTATAAATGACCGTATTATAACATTTGAAAAAGTCTT  
CATCAAAAAAAAAAAAAAA



474/615

**FIGURE 470**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA80136
><subunit 1 of 1, 209 aa, 1 stop
><MW: 23909, pI: 9.68, NX(S/T): 0
MEPLAAYPLKCSGPRAKVFAVLLSIVLCTVTLFLLQLKFLKPKINSFYAFEVKDAKGRTVSLE
KYKGKVSLLVNVASDCQLTDRNYLGLKELHKEFGPSHFVLAFFPCNQFGESEPRPSKEVESFA
RKNYGVTFPFIHFKIKILGSEGEPAFRFLVDSSKKEPRWNFWKYLVNPEGQVVKFWRPEEPIEV
IRPDIAALVRQVVIKKKEDL
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-31

**Glutathione peroxidases signature 2.**

amino acids 104-112

**Glutathione peroxidases.**

amino acids 57-82

475/615

**FIGURE 471**

GCCCTAACCTTCCCAGGGCTCAGCTCTTTGGAGCTGCCCATTCCTCCGGCTGCGAGAAAGGACGCGCGCCCTGCG  
TCGGGCGAAGAAAAGAAGCAAACTTGTGCGGAGGGTTTCGTCAACCTCCTTCCCAGAACTAACCTCCT  
GCCGGGGCCATCCCTAGACAGAGGAAAGTTCCTGCAGAGCCGACCAGCCCTAGTGGATCTGGGGCAGGCAGCGGC  
GCTGGCTGTGGAATTAGATCTGTTTTGAACCCAGTGGAGCGCATCGCTGGGGCTCGGAAGTCACCGTCCGCGGGC  
ACCGGGTTGGCGCTGCCCAGTGGAAACCGACAGTTTGGCAGCCTCGGCTGCAAGTGGCCTCTCCTCCCCGCGGTT  
GTTGTTTCAGTGTGCGGTGAGGGCTGCGAGTGTGGCAAGTTGCAAAGAGAGCCTCAGAGGTCCGAAGAGCGCTGCG  
CTCCTACTCGCGTTGCTTCTTCTCTCGGTTCCCTACTGTGAAATCGCAGCGACATTTACAAAGGCCTCCG  
GGTCTACCGAGACCGATCCGCAGCGTTTGGCCCGGTCGTGCCTATTGCATCGGGAGCCCCGAGCACCGGCGAA  
GGACTGGCGGGTGGGGTAGGGAGGTGGCGGGCGGCGCATGGCGAGGTTCCCGAAGGCCGACCTGGCCGCTGCAGG  
AGTTATGTTACTTTGCCACTTCTTCACGGACCAAGTTTCAGTTCGCCGATGGGAAACCCGGAGACCAATCCTTGA  
TTGGCAGTATGGAGTTACTCAGGCCTTCCCTCACACAGAGGAGGAGGTGGAAGTTGATTCACACGCGTACAGCCA  
CAGGTGGAAAAGAACTTGGACTTTCTCAAGGCGGTAGACACGAACCGAGCAAGCGTCGGCCAAGACTCTCCTGA  
GCCAGAAGCTTCACAGACCTGCTGCTGGATGATGGGCAGGACAATAACACTCAGATCGAGGAGGATACAGACCA  
CAATTACTATATATCTCGAATATATGGTCCATCTGATTCTGCCAGCCGGGATTTATGGGTGAACATAGACCAAT  
GGAAAAGATAAAGTGAAGATTTCATGGAATATTGTCCAATACTCATCGGCAAGCTGCAAGAGTGAATCTGTCTT  
CGATTTTCCATTTTATGGCCACTTCTTACGTGAAATCACTGTGGCAACCGGGGGTTTCATATACACTGGAGAAGT  
CGTACATCGAATGCTAACAGCCACACAGTACATAGCACCTTTAATGGCAAATTCGATCCCAGTGTATCCAGAAA  
TTCAACTGTGAGATATTTTGATAATGGCACAGCACTTGTGGTCCAGTGGGACCATGTACATCTCCAGGATAATTA  
TAACCTGGGAAGCTTCACATTCCAGGCAACCTGCTCATGGATGGACGAATCATCTTTGGATACAAAGAAATTCC  
TGTCTGGTCACACAGATAAGTTCAACCAATCATCCAGTGAAGTCCGACTGTCCGATGCATTTGTCGTTGTCCA  
CAGGATCCAACAAATTCCCAATGTTGGAAGAAGAACAATTTATGAATACCACCGAGTAGAGCTACAAATGTCAAA  
AATTACCAACATTTCCGGCTGTGGAGATGACCCATTACCCACATGCCTCCAGTTTAAACAGATGTGGCCCCCTGTGT  
ATCTTCTCAGATTGGCTTCACTGCAGTTGGTGTAGTAACTTCAAAGATGTTCCAGTGGATTTGATCGTCATCG  
GCAGGACTGGGTGGACAGTGGATGCCCTGAAGAGTCAAAGAGAGAAGATGTGTGAGAATACAGAACCAGTGGAAAC  
TTCTTCTCGAACCACCACAACCGTAGGAGCGACAACCACCCAGTTCAGGGTCCTAACTACCACCAGAAGAGCAGT  
GACTTCTCAGTTTCCCACCAGCCTCCCTACAGAAGATGATACCAAGATAGCACTACATCTAAAAGATAATGGAGC  
TTCTACAGATGACAGTGCAGCTGAGAAGAAAGGGGAACCCCTCCACGCTGGCCTCATCATTGGAATCCTCATCCT  
GGTCTCATTGTAGCCACAGCCATTCTTGTGACAGTCTATATGTATCACCACCCAACATCAGCAGCCAGCATCTT  
CTTTATTGAGAGACGCCCAGCAGATGGCCTGCGATGAAGTTTGAAGAGGCTCTGGACATCCTGCCTATGCTGA  
AGTTGAACCAGTTGGAGAGAAAGAAGGCTTTATTGTATCAGAGCAGTGCATAAAATTTCTAGGACAGAACAACACC  
AGTACTGGTTTACAGGTGTTAAGACTAAAATTTTGCCTATACCTTTAAGACAAACAAACACACACACAAAC  
AAGCTCTAAGCTGCTGTAGCCTGAAGAAGACAAGATTTCTGGACAAGCTCAGCCCAGGAAACAAAGGGTAAACAA  
AAAATAAACTTATACAAGATACCATTTACACTGAACATAGAATTCCCTAGTGGAAATGTCATCTATAGTTCACT  
CGGAACATCTCCCGTGGACTTATCTGAAGTATGACAAGATTATAATGCTTTTGGCTTAGGTGCAGGTTGCAAAG  
GGATCAGAAAAAAAATCATAATAAGCTTTAGTTCATGAGG

476/615

**FIGURE 472**

MARFPKADLAAAGVMLLCHFFTDQFQFADGKPGDQILDWQYGVTOAFPHTEEVEVDSHAYSH  
RWKRNLDFLKAVDTNRASVGQDSPEPRSFTDLLDDGQDNNTQIEEDTDHNYIISRIYGPSDS  
ASRDLWVNIDQMEKDKVKIHGILSNTHRQAARVNLSFDFPFYGHFLREITVATGGFIYTGEVV  
HRMLTATQYIAPLMANFDPSSVRNSTVRYFDNGTALVVQWDHVLQDNYNLGSFTFQATLLMD  
GRIIFGYKEIPVLVTQISSTNHPVKVGLSDAFVVVHRIQQIPNVRRTIYEHVRELQMSKIT  
NISAVEMTPLPTCLQFNRCGPCVSSQIGFNCSWCSKLRQCSSGFDHRQDWVDSGCPEESKEK  
MCENTEPVETSSRTTTTGVGATTQFRVLTTTTRAVTSQFPTSLPTEDDTKIALHLKDNASTD  
DSAAEKKGGTLHAGLIIGILILVLIVATAILVTVYMYHHPTSAASIFFIERRPSRWPAMKFRR  
GSGHPAYAEVEPVGEKEGFIVSEQC

**Important features of the protein:****Transmembrane domain:**

amino acids 454-478

**N-glycosylation sites.**

amino acids 103-107, 160-164, 213-217, 221-225, 316-320, 345-349

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 297-301, 492-496, 503-507

**N-myristoylation sites.**amino acids 42-48, 100-106, 147-153, 279-285, 397-403, 450-456,  
455-461

477/615

**FIGURE 473**

CGCGGAGCCCTGCGCTGGGAGGTGCACGGTGTGCACGCTGGACTGGACCCCCATGCAACCCCG  
CGCCCTGCGCCTTAACCAGGACTGCTCCGCGCGCCCTGAGCCTCGGGCTCCGGCCCGGACCT  
GCAGCCTCCCAGGTGGCTGGGAAGAACTCTCCAACAATAAATACATTTGATAAGAAAGATGGC  
TTTAAAGTGCTACTAGAACAAAGAGAAAACGTTTTTCACTCTTTTAGTATTACTAGGCTATTT  
GTCATGTAAAGTGACTTGTGAATCAGGAGACTGTAGACAGCAAGAATTCAGGGATCGGTCTGG  
AAACTGTGTTCCCTGCAACCAGTGTGGGCCAGGCATGGAGTTGTCTAAGGAATGTGGCTTCGGC  
TATGGGGAGGATGCACAGTGTGTGACGTGCCGGCTGCACAGGTTCAAGGAGGACTGGGGCTTC  
CAGAAATGCAAGCCCTGTCTGGACTGCGCAGTGGTGAACCGCTTTCAGAAGGCAAATTGTTCA  
GCCACCAGTGATGCCATCTGCGGGGACTGCTTGCCAGGATTTTATAGGAAGACGAAACTTGTG  
GGCTTTCAAGACATGGAGTGTGTGCCTTGTGGAGACCCTCCTCCTTACGAACCGCACTGT  
GCCAGCAAGGTCAACCTCGTGAAGATCGCGTCCACGGCCTCCAGCCCACGGGACCGGCGTG  
GCTGCCGTTATCTGCAGCGCTCTGGCCACCGTCTGCTGGCCCTGCTCATCCTCTGTGTATC  
TATTGTAAGAGACAGTTTATGGAGAAGAAACCCAGCTGGTCTCTGCGGTGCGAGGACATTGAG  
TACAACGGCTCTGAGCTGTGCTGTTTTGACAGACCTCAGCTCCACGAATATGCCACAGAGCC  
TGCTGCCAGTGCCGCCGTGACTCAGTGCAGACCTGCGGGCCGGTGCCTTGTCTCCATCCATG  
TGCTGTGAGGAGGCCTGCAGCCCCAACCCGGCGACTCTTGGTTGTGGGGTGCATTCTGCAGCC  
AGTCTTCAGGCAAGAAACGCAGGCCAGCCGGGGAGATGGTGCCGACTTTCTTCGGATCCCTC  
ACGCAGTCCATCTGTGGCGAGTTTTTCAGATGCCTGGCCTCTGATGCAGAATCCCATGGGTGGT  
GACAACATCTCTTTTTGTGACTCTTATCCTGAACTCACTGGAGAAGACATTCTCTCTCAAT  
CCAGAACTTGAAAGCTCAACGTCTTTGGATTCAAATAGCAGTCAAGATTTGGTTGGTGGGGCT  
GTTCCAGTCCAGTCTCATTCTGAAAACCTTACAGCAGCTACTGATTTATCTAGATATAACAAC  
ACACTGGTAGAATCAGCATCAACTCAGGATGCACTAACTATGAGAAGCCAGCTAGATCAGGAG  
AGTGGCGCTGTATCCACCCAGCCACTCAGACGTCCCTCCAGGAAGCTTAAAGAACCTGCTTC  
TTTCTGCAGTAGAAGCGTGTGCTGGAACCCAAAGAGTACTCCTTTGTTAGGCTTATGGACTGA  
GCAGTCTGGACCTTGCATGGCTTCTGGGGCAAAAATAAATCTGAACCAAACCTGACGGCATTG  
AAGCCTTTCAGCCAGTTGCTTCTGAGCCAGACCAGCTGTAAGCTGAAACCTCAATGAATAACA  
AGAAAAGACTCCAGGCCGACTCATGATACTCTGCATCTTTCCTACATGAGAAGCTTCTCTGCCAC  
AAAAGTGACTTCAAAGACTGATGGGTTGAGCTGGCAGCCTATGAGATTGTGGACATATAACAA  
GAAACAGAAATGCCCTCATGCTTATTTTCATGGTGATTGTGGTTTTACAAGACTGAAGACCCA  
GAGTATACTTTTTCTTTCCAGAAATAATTTACATACCGCCTATGAAATATCAGATAAATTACCT  
TAGCTTTTATGTAGAATGGGTTCAAAGTGAGTGTCTTCTATTTGAGAAGGACACTTTTTCATC  
ATCTAAACTGATTTCGCATAGGTGGTTAGAATGGCCCTCATATTGCCTGCCTAAATCTTGGGTT  
TATTAGATGAAGTTTACTGAATCAGAGGAATCAGACAGAGGAGGATAGCTCTTTCAGAAATCC  
ACACTTCTGACCTCAGCCTCGGTCTCATGAACACCCGCTGATCTCAGGAGAACACCTGGGCTA  
GGGAATGTGGTCGAGAAAGGGCAGCCCATGCCCAGAATTAACACATATTGTAGAGACTTGTA  
TGCAAAGGTTGGCATATTTATATGAAAATTAGTTGCTATAGAAACATTTGTTGCATCTGTCCC  
TCTGCCTGAGCTTAGAAGGTTATAGAAAAAGGGTATTTATAAACATAAATGACCTTTTACTTG  
CATTGTATCTTATACTAAAGGCTTTAGAAATTACAACATATCAGGTTCCCTACTACTGAAGT  
AGCCTTCCGTGAGAACACACCACATGTTAGGACTAGAAGAAAATGCACAATTTGTAGGGGTTT  
GGATGAAGCAGCTGTAACCTGCCCTAGTGTAGTTTGACCAGGACATTGTCGTGCTCCTTCCAAT  
TGTGTAAGATTAGTTAGCACATCATCTCTACTTTAGCCATCCGGTGTGGATTTAAGAGGAC  
GGTGCTTCTTTCTATTAAAGTGCTCCATCCCCTACCATCTACACATTAGCATTTGTCTCTAGAG  
CTAAGACAGAAATTAACCCCGTTCAAGTCACAAAGCAGGGAATGGTTCATTTACTCTTAATCTT  
TATGCCCTGGAGAAGACCTACTTGAACAGGGCATATTTTTTAGACTTCTGAACATCAGTATGT  
TCGAGGGTACTATGATATTTTGGTTTGAATTGCCCTGCCCAAGTCACTGTCTTTTAACTTTT  
AAACTGAATATTAAATGTATCTGTCTTTCCT

478/615

**FIGURE 474**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA84210
><subunit 1 of 1, 417 aa, 1 stop
><MW: 45305, pI: 5.12, NX(S/T): 6
MALKVLLLEQEKTFFTLLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSK
ECGFGYGEDAQCVCRLHRFKEDWGFQKCKPCLDCAVVNRFAQKANCSDAICGDCLPG
FYRKTKLVGFQDMECVPCGDP PPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT
VLLALLILCVIYCKRQFMKKPSWSLRSQDIQYNGSELSCFDRPQLHEYAHRACCQCRD
SVQTCGPVRLLLPSMCCEEACSPNPATLGCGVHSAASLQARNAGPAGEMVPTFFGSLTQSI
CGEFSDAWPLMQNPMGGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV
PVQSHSENFATAATDLSRYNNTLVESASTQDALTMRSQLDQESGAVIHPATQTSLQEA
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-25

**Transmembrane domain:**

Amino acids 169-192

**N-glycosylation sites:**

Amino acids 105-109;214-218;319-323;350-354;368-372;379-383

**cAMP- and cGMP-dependent protein kinase phosphorylation sites:**

Amino acids 200-204;238-242

**Tyrosine kinase phosphorylation site:**

Amino acids 207-214

**N-myristoylation sites:**

Amino acids 55-61;215-221;270-276

**Prokaryotic membrane lipoprotein lipid attachment site:**

Amino acids 259-270

**TNFR/NGFR family cysteine-rich region proteins:**

Amino acids 89-96

479/615

**FIGURE 475**

AGCCAGGCAGCACATCACAGCGGGAGGAGCTGTCCCAGGTGGCCCAGCTCAGCA**ATG**GCAATG  
GGGGTCCCCAGAGTCATTCTGCTCTGCCTCTTTGGGGCTGCGCTCTGCCTGACAGGGTCCCAA  
GCCCTGCAGTGCTACAGCTTTGAGCACACCTACTTTGGCCCCTTTGACCTCAGGGCCATGAAG  
CTGCCCAGCATCTCCTGTCCTCATGAGTGCTTTGAGGCTATCCTGTCTCTGGACACCGGGTAT  
CGCGCGCCGGTGACCCTGGTGCGGAAGGGCTGCTGGACCGGGCCTCCTGCGGGCCAGACGCAA  
TCGAACCCGGACGCGCTGCCGCCAGACTACTCGGTGGTGCGCGGCTGCACAACTGACAAATGC  
AACGCCCACCTCATGACTCATGACGCCCTCCCCAACCTGAGCCAAGCACCCGACCCGCCGACG  
CTCAGCGGCGCCGAGTGCTACGCCTGTATCGGGGTCCACCAGGATGACTGCGCTATCGGCAGG  
TCCCGACGAGTCCAGTGTCACCAGGACCAGACCGCCTGCTTCCAGGGCAGTGGCAGAATGACA  
GTTGGCAATTTCTCAGTCCCTGTGTACATCAGAACCTGCCACCGGCCCTCCTGCACCACCGAG  
GGCACCACCAGCCCCTGGACAGCCATCGACCTCCAGGGCTCCTGCTGTGAGGGGTACCTCTGC  
AACAGGAAATCCATGACCCAGCCCTTCACCAGTGCTTCAGCCACCACCCCTCCCCGAGCACTA  
CAGGTCCTGGCCCTGCTCCTCCCAGTCCTCCTGCTGGTGGGGCTCTCAGCA**TAG**ACCGCCCCCT  
CCAGGATGCTGGGGACAGGGCTCACACACCTCATTCTTGCTGCTTCAGCCCCTATCACATAGC  
TCACTGGAAAATGATGTTAAAGTAAGAATTGCAAAA

480/615

**FIGURE 476**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA86576
><subunit 1 of 1, 251 aa, 1 stop
><MW: 26935, pI: 7.42, NX(S/T): 2
MAMGVPRVILLCLFGAALCLTGSQALQCYSFEHTYFGPFDLRAMKLPSISCPHECFEAILSLD
TGYRAPVTILVRKGCWTGPPAGQTQSNPDALPPDYSVVRGCTTDKCNAHLMTHDALPNLSQAPD
PPTLSGAECYACIGVHQDDCAIGRSRRVQCHQDQTACFQSGRMTVGNFSVPVYIRTCHRPSC
TTEGTTSPWTAIDLQGSCEGYLCNRKSMTQPFTSASATTPPRALQVLALLLPVLLLVGLSA
```

**Important features of the protein:****Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 233-251

**N-glycosylation sites.**

amino acids 120-124, 174-178

**N-myristoylation sites.**

amino acids 15-21, 84-90

481/615

**FIGURE 477**

CCCACGCGTCCGGGACAGATGAACTTAAAGAGAAGCTTTAGCTGCCAAAGATTGGGAAAGGGAAAGGACAAAA  
AGACCCCTGGGCTACACGGCGTAGGTGCAGGGTTTCTACTGCTGTTCTTTTATGCTGGGAGCTGTGGCTGTAAC  
CAACTAGGAAATAACGTATGCAGCAGCTATGGCTGTCAGAGAGTTGTGCTTCCCAAGACAAAGGCAAGTCTCTGT  
TCTTTTTCTTTTTTGGGGAGTGTCTTGGCAGGTTCTGGGTTTGGACGTTATTCCGGTGAAGTGAAGAAACAGAGAA  
AGGATCCTTTGTGGTCAATCTGGCAAAGGATCTGGGACTAGCAGAGGGGGAGCTGGCTGCAAGGGGAACCAGGGT  
GGTTTCCGATGATAACAAACAATACCTGCTCCTGGATTACATACCGGGAATTTGCTCACAAATGAGAACTGGA  
CCGAGAGAAGCTGTGTGGCCCTAAAGAGCCCTGTATGCTGTATTTCCAAATTTTAAATGGATGATCCCTTTCAGAT  
TTACCGGGCTGAGCTGAGAGTCAGGGATATAAATGATCAGCGCCAGTATTTCCAGGACAAAGAAACAGTCTTAAA  
AATATCAGAAAATACAGCTGAAGGGACAGCATTTAGACTAGAAAGAGCACAGGATCCAGATGGAGGACTTAACGG  
TATCCAAAATACACGATCAGCCCCAATCTTTTTTCCATATTAACATTAGTGGCGGTGATGAAGGCATGATATA  
TCCAGAGCTAGTGTTGGACAAAGCACTGGATCGGGAGGAGCAGGGAGAGCTCAGCTTAACCCCTCACAGCGCTGGA  
TGGTGGGTCTCCATCCAGGTCTGGGACCTCTACTGTACGCATCGTTGTCTTGGACGTCAATGACAATGCCCCACA  
GTTTGGCCAGGCTCTGTATGAGACCCAGGCTCCAGAAAACAGCCCCATTGGGTTCTTATTGTTAAGGTATGGGC  
AGAAGATGTAGACTCTGGAGTCAACGCGGAAGTATCCTATTCTTTTTTGTGCTCAGAAAATATTTCGAACGAC  
CTTTCAAATCAATCCTTTTTCTGGGAAATCTTCTCAGAGAATTGCTTGATTATGAGTTAGTAAATCTTACAA  
AATAAATATACAGGCAATGGACGGTGGAGGCCTTTCTGCAAGATGTAGGGTTTTAGTGAAGTATTGGACACCAA  
TGACAATCCCCCTGAATGATCGTATCATCTTTTCCAACTCTGTTGCTGAGAATTCTCCTGAGACGCCGCTGGC  
TGTTTTTAAGATTAATGACAGAGACTCTGGAGAAAATGGAAGATGGTTTGCTACATTCAAGAGAATCTGCCATT  
CCTACTAAAACCTTCTGTGGAGAATTTTACATCCTAATTACAGAAGGCGCGCTGGACAGAGAGATCAGAGCCGA  
GTACAACATCACTATCACCCTCACTGACTTGGGACACCCAGGCTGAAAACCGAGCACAAACATAACGGTCTGGT  
CTCCGACGTCAATGACAACGCCCGCCCTTACCCAAACCTCTACACCCTGTTCTGTCGCGGAGAACACAGCCC  
CGCCCTGCACATCGGCAGCGTCAGCGCCACAGACAGAGACTCGGGCACCAACGCCAGGTACCTACTCGCTGCT  
GCCGCCCAAGACCCGACCTGCCCTCGCCTCCCTGGTCTCCATCAACGCGGACAACGGCCACCTGTTCCGCCCT  
CAGTCTGCTGGACTACGAGGCCCTGCAGGCTTTCGAGTTCGCGCTGGGCGCCACAGACCCGCGCTCCCCCGCGCT  
GAGCAGAGAGGCGCTGGTGCCTGCTGGTGGTGGACGCCAACGACAACCTCGCCCTTCTGCTGTACCCGCTGCA  
GAACGGCTCCGCGCCCTGCACCGAGCTGGTGGCCCGGGCGCGGAGCCGGGTACCTGGTGACCAAGGTGGTGGC  
GGTGGACGGCGACTCGGGCCAGAACGCCTGGCTGTCTGACAGCTGCTCAAGGCCACGGAGCCCGGGTGTTCGG  
TGTGTGGGCGCACAAATGGGGAGGTGCGCACCGCCAGGCTGCTGAGCGAGCGCGACGCAGCCAAGCACAGGCTCGT  
GGTGTGTTGTCAAGGACAATGGCGAGCCTCCTCGCTCGGCCACCGCCACGCTGCATTGCTCCTGGTGGACGGCTT  
CTCCAGCCCTACCTGCCTCTCCCGAGGCGGCCCGGCCAGGCCAGGCCGAGGCCGACTTGCTCACCGTCTA  
CCTGGTGGTGGCGTTGGCCTCGGTGTCTTCGCTCTTCTCCTCTCGGTGCTCCTGTTCTGTCGGGCTGTG  
CAGGAGGAGCAGGGCGGCCCTCGGTGGGTGCTGCTCGGTGCCGAGGGTCTTTTTCCAGGGCATCTGGTGGACGT  
GAGGGGCGCTGAGACCTGTCCCAGAGCTACCAGTATGAGGTGTGTCTGACGGGAGGCCCCGGGACCAAGTGA  
CAAGTTCTTGAAACAGTTATTTTCGGATATTCAGGCACAGGGCCCTGGGAGGAAGGTGAAGAAAATTCACCTT  
CCGAAATAGCTTTGGATTTAATATTTCAGTAAAGTCTGTTTTTAGTTTCATATACTTTTGGTGTGTTACATAGCCA  
TGTTTCTATTAGTTTACTTTTAAATCTCAAATTTAAGTTATTATGCAACTTCAAGCATTATTTTCAAGTAGTATA  
CCCCTGTGGTTTTACAATGTTTCATCATTTTTTTGCATTAAATAACAATGGGTTTAAATTAATGAGTATTTTTT  
CTAAATGATAGTGTTAAGGTTTTAATCTTTTCCAACTGCCCAAGGAATTAATTACTATTATATCTCATTACAGAA  
ATCTGAGGTTTTGATTCATTTAGAGCTTGCATCTCATGATTCTAATCACTTCTGTCTATAGTGTACTTGTCTTA  
TTTAAGAAGGCATATCTACATTTCCAACTCATTCTAATCTATATATTCGTGTTTGAACCATGTCAATTTA  
TTTCTACATCATGTATTTAAAAAGAAATATTTCTCTACTACTATGCTCATGACAAATGAAACAAAGCATATTGT  
GAGCAATACTGAACATCAATAATACCTTAGTTTATATACTTATTATTTTATCTTTAAGCATGCTACTTTTACTT  
GGCCAATATTTTCTTATGTTAACTTTTGCTGATGTATAAAACAGACTATGCCTTATAATTGAAATAAAATTATAA  
TCTGCCTGAAATGAATAAAAAATAAACATTTGAAATGTGAAAAAATAAAAAAAAAAAAAA



482/615

**FIGURE 478**

&gt;&lt;/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA87976

&gt;&lt;subunit 1 of 1, 800 aa, 1 stop

&gt;&lt;MW: 87621, pI: 4.77, NX(S/T): 7

MAVRELCFPRQVLFLLFWGVSLAGSGFGGRYSVTEETEGKGSFVVNLAKDLGLAEGELAARG  
 TRVVSDDNKQYLLLDSTGNLLTNEKLDREKLCGPKEPCMLYFQILMDDPFQIYRAELRVRDI  
 NDHAPVFQDKETVLKISENTAEGTAFRLERAQDPDGGGLNGIQNYTISPNSFFHINISGGDEGM  
 IYPELVLDKALDREEQGELSLTLTALDGGSPSRSGTSTVRIVLDVNDNAPQFAQALYETQAP  
 ENSPIGFLIVKVWAEDVDSGVNAEVSYSFFDASENIRTTTFQINPFSGEIFLRELLDYELVNSY  
 KINIQAAMDGGGLSARCRVLVEVLDTNDNPPELIVSSFSNSVAENSPETPLAVFKINDRDSGEN  
 GKMVCYIQENLPFLKPSVENFYILITEGALDREIRAEYNITITVTDLGTPRLKTEHNITVLV  
 SDVNDNAPAFQTQTSYTLFVRENNSPALHIGSVSATDRDSGTNAQVTYSLLPPQDPHLPLASLV  
 SINADNGHLFALRSLDYEALQAFEFVRGATDRGSPALSREALVRVLVDANDNSPFVLYPLQN  
 GSAPCTELVPRAAEPGYLVTKVVAVDGDSGQNAWLSYQLLKATEPGLFGVWAHNGEVRTARLL  
 SERDAAKHRLVVLVKDNGEPPRSATATLHLLLVDGFSQPYLPLPEAAPAQAEADLLTVYLV  
 VALASVSSLFLLSVLLFVAVRLCRRSRAASVGRCSVPEGPFPGHLVDVRGAETLSQSYQYEV  
 LTGGPGTSEFKFLKPVISDIQAQGPGRKGEENSTFRNSFGFNIQ

**Important features of the protein:****Signal peptide:**

amino acids 1-26

**Transmembrane domain:**

amino acids 687-711

**N-glycosylation sites.**

amino acids 169-173, 181-185, 418-422, 436-440, 567-571, 788-792

**Glycosaminoglycan attachment site.**

amino acids 28-32

**Tyrosine kinase phosphorylation sites.**

amino acids 394-402, 578-585

**N-myristoylation sites.**amino acids 22-28, 27-33, 53-59, 82-88, 162-168, 184-190,  
217-223, 324-330, 325-331, 471-477, 568-574, 759-765**Amidation site.**

amino acids 781-785

**Aminoacyl-transfer RNA synthetases class-II signature 1.**

amino acids 117-138

**Cadherins extracellular repeated domain signature.**

amino acids 121-132, 230-241, 335-346, 439-450, 549-560

483/615

**FIGURE 479**

CTCGGCTGGATTTAAGGTTGCCGCTAGCCGCCTGGGAATTTAAGGGACCCACACTACCTTCCC  
GAAGTTGAAGGCAAGCGGTGATTGTTTGTAGACGGCGCTTTGTCA**ATG**GGACCTGTGCGGTTGG  
GAATATTGCTTTTTCCTTTTTTTGGCCGTGCACGAGGCTTGGGCTGGGATGTTGAAGGAGGAGG  
ACGATGACACAGAACGCTTGCCACGAAATGCCAAGTGTGTAAGCTGCTGAGCACAGAGCTAC  
AGGCGGAAGTGAAGTCGCACCGGTCGATCTCGAGAGGTGCTGGAGCTGGGGCAGGTGCTGGATA  
CAGGCAAGAGGAAGAGACACGTGCCTTACAGCGTTTCAGAGACAAGGCTGGAAGAGGCCTTAG  
AGAATTTATGTGAGCGGATCCTGGACTATAGTGTTACGCTGAGCGCAAGGGCTCACTGAGAT  
ATGCCAAGGGTCAGAGTCAGACCATGGCAACACTGAAAGGCCTAGTGAGAAGGGGGTGAAGG  
TGGATCTGGGGATCCCTCTGGAGCTTTGGGATGAGCCCAGCGTGGAGGTACATACCTCAAGA  
AGCAGTGTGAGACCATGTTGGAGGAGTTTGAAGACATTGTGGGAGACTGGTACTTCCACCATC  
AGGAGCAGCCCCCTACAAAATTTTCTCTGTGAAGGTCATGTGCTCCCAGCTGCTGAAACTGCAT  
GTCTACAGGAAACTTGGACTGGAAAGGAGATCACAGATGGGGAAGAGAAAACAGAAGGGGAGG  
AAGAGCAGGAGGAGGAGGAGGAAGAGGAGGAAGAGGAAGGGGGAGACAAGATGACCAAGACAG  
GAAGCCACCCCAAACCTTGACCGAGAAGATCTT**TGA**CCCTTGCCTTTGAGCCCCCAGGAGGGGA  
AGGGATCATGGAGAGCCCTCTAAAGCCTGCACTCTCCCTGCTCCACAGCTTTCAGGGTGTGTT  
TATGAGTGACTCCACCCAAGCTTGTAAGCTGTTCTCTCCCATCTAACCTCAGGCAAGATCCTGG  
TGAAACAGCATGACATGGCTTCTGGGGTGGAGGGTGGGGGTGGAGGTCTGCTCCTAGAGATG  
AACTCTATCCAGCCCCCTTAATTGGCAGGTGTATGTGCTGACAGTACTGAAAGCTTTCCTCTTT  
AACTGATCCACCCCCACCCAAAAGTCAGCAGTGGCACTGGAGCTGTGGGCTTTGGGGAAGTC  
ACTTAGCTCCTTAAGGTCTGTTTTTAGACCCTTCCAAGGAAGAGGCCAGAACGGACATTCTCT  
GCGATCTATATACATTGCCTGTATCCAGGAGGCTACACACCAGCAAACCGTGAAGGAGAATGG  
GACACTGGGTGATGGCCTGGAGTTGCTGATAATTTAGGTGGGATAGATACTTGGTCTACTTAA  
GCTCAATGTAACCCAGAGCCACCATATAGTTTTATAGGTGCTCAACTTCTATATCGCTATT  
AAACTTTTTTCTTTTTTTCTA

484/615

**FIGURE 480**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA92256  
><subunit 1 of 1, 248 aa, 1 stop  
><MW: 28310, pI: 4.63, NX(S/T): 0  
MGPVRLGILLFLFLAVHEAWAGMLKEEDDDTERLPSKCEVCKLLSTELQAELSRTGRSREVLE  
LGQVLDTGKRKRHVPYSVSETRLEEALENLCERILDYSVHAERKGSRLRYAKGQSQTMTATLKGL  
VQKGVKVDLGIPLELWDEPSVEVITYLKKQCETMLEEFEDIVGDWYFHHQEQLQNFLCEGHVL  
PAAETACLQETWTGKEITDGEKTEGEEEQEEEEEEEEEGGDKMTKTGSHPKLDREDL

**Important features of the protein:****Signal peptide:**

amino acids 1-21

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 106-110

**N-myristoylation site.**

amino acids 115-121

**Amidation site.**

amino acids 70-74

485/615

**FIGURE 481**

GGCGTGTGCAAGGCGGGGTCCGGCCCGCGCAGGTGGGTAAGCGCGTCTAGGGCGCTGCGCGG  
CGCAGCGAAAATGGCGGCTTCCAGGTGGGCGCGCAAGGCCGTGGTCCTGCTTTGTGCCTCTGA  
CCTGCTGCTGCTGCTGCTACTGCTACCAACCGCCTGGGTCTGCGCGGCCGAAGGCTCGCCCGG  
GACGCCCCGACGAGTCTACCCACCTCCCCGGAAGAAGAAGGATATTGCGGATTACAATGA  
TGCAGACATGGCGCGTCTTCTGGAGCAATGGGAGAAAGATGATGACATTGAAGAAGGAGATCT  
TCCAGAGCACAAGAGACCTTCAGCACCTGTCGACTTCTCAAAGATAGACCCAAGCAAGCCTGA  
AAGCATATTGAAAATGACGAAAAAAGGGAAGACTCTCATGATGTTTGTCACTGTATCAGGAAG  
CCCTACTGAGAAGGAGACAGAGGAAATTACGAGCCTCTGGCAGGGCAGCCTTTTCAATGCCAA  
CTATGACGTCCAGAGGTTTCAATTGTGGGATCAGACCGTGCTATCTTCATGCTTCGCGATGGGAG  
CTACGCCTGGGAGATCAAGGACTTTTTTGGTCGGTCAAGACAGGTGTGCTGATGTAACCTGGA  
GGGCCAGGTGTACCCCGGCCAAAGGAGGAGGAAGCAAAGAGAAAAATAAAACAAAGCAAGACAA  
GGGCAAAAAAAGAAGGAAGGAGATCTGAAATCTCGGTCTTCCAAGGAAGAAAATCGAGCTGG  
GAATAAAAGAGAAGACCTGTGATGGGGCAGCAGTGACGCGCTGTGGGGGGACAGGTGGACGTG  
GAGAGCTCTTTGCCAGCTCCTGGGGTGGGAGTGGTCTCAGGCAACTGCACACCGGATGACAT  
TCTAGTGTCTTCTAGAAAAGGTCTGCCACATGACCAGTTTGTGGTCAAAGAATTACTGCTTAA  
TAGGCTTCAAGTAAGAAGACAGATGTTTTCTAATTAATACTGGACACTGACAAATTCATGTTT  
ACTATAAAATCTCCTTACATGGAAATGTGACTGTGTTGCTTTTTTCCATTTTACACTTGGTGAG  
TCATCAACTCTACTGAGATTCCACTCCCCTCCAAGCACCTGCTGTGATTGGGTGGCCTGCTCT  
GATCAGATAGCAAATTCATGATCAGAGAAGACTTTAAACTCTTGACTTAATTGAGTAACTCT  
TCATGCCATATACATCATTTTCATTATGTTAAAGGTAAAATATGCTTTGTGAACTCAGATGTC  
TGTAGCCAGGAAGCCAGGGTGTGTAAATCCAAATCTATGCAGGAAATGCGGAGAATAGAAAA  
TATGTCACCTTGAAATCCTAAGTAGTTTTGAATTTCTTTGACTTGAATCTTACTCATCAGTAAG  
AGAACTCTTGGTGTCTGTCAGGTTTTATGTGGTCTGTAAAGTTAGGGGTTCTGTTTTGTTTCC  
TTATTTAGGAAAGAGTACTGCTGGTGTGAGGGGTTATATGTTCCATTTAATGTGACAGTTTT  
AAAGGATTTAAGTAGGGAATCAGAGTCCTTTGCAGAGTGTGACAGACGACTCAATAACCTCAT  
TTGTTTCTAAACATTTTTCTTTGATAAAGTGCCTAAATCTGTGCTTTCGTATAGAGTAACATG  
ATGTGCTACTGTTGATGTCTGATTTTGCCGTTCATGTTAGAGCCTACTGTGAATAAGAGTTAG  
AACATTTATATACAGATGTCATTTCTAAGAACTAAAATTCCTTTGGGAAAAACCCTCAAAAAA  
AAAAAAAAAAAAAAAAAAAAA

486/615

**FIGURE 482**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA92289
><subunit 1 of 1, 234 aa, 1 stop
><MW: 26077, pI: 8.13, NX(S/T): 1
MAASRWARKAVVLLCASDLLLLLLLLLPPPGSCAAEGSPGTPDESTPPPRKKKKDIRDYND
ADMARLLEQWEKDDDDIEEGDLPEHKRPSAPVDFSKIDPSKPESILKMTKKGKTLMMFVTV
SGSPTEKETEEITSLWQGSLEFNANYDVQRFIVGSDRAIFMLRDGSYAWWEIKDFLVGQDRC
ADVTLEGQVYPGKGGSKEKNKTKQDKGKKKKEGDLKSRSSKEENRAGNKREDL
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-32

**N-glycosylation site:**

Amino acids 201-205

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 85-89

**Tyrosine kinase phosphorylation site:**

Amino acids 50-59

**N-myristoylation sites:**

Amino acids 30-36;138-144;153-159;176-182

**Amidation site:**

Amino acids 207-211

**FIGURE 483**

[illegible]

488/615

**FIGURE 484**

MALPPGPAALRHTLLLLPALLSSGWGELEPQIDGQTWAERALRENERHAFTCRVAGGPGTPRL  
AWYLDGQLQEASTSRLLSVGGEAFSGGTSTFTVTAHRAQHELNCSLQDPRSGRSANASVILNV  
QFKPEIAQVGAKYQEAQGPGLLVVLFALVRANPPANVTWIDQDGPVTVNTSDFLVLDAQNYPW  
LTNHTVQLQLRSLAHNLSVVATNDVGVTASLPAPGPSRHPSLISSDSNNLKLNNVRLPRENM  
SLPSNLQLNDLTPDSRAVKPADRQMAQNNSRPELLDPEPGGLLTSQGFIRLPVLGYIYRVSSV  
SSDEIWL

**N-glycosylation sites:**

amino acids 106-110, 119-123, 162-166, 175-179, 192-196, 205-209,  
251-255, 280-284

**Glycosaminoglycan attachment site:**

amino acids 23-27

**Casein kinase II phosphorylation sites:**

amino acids 36-40, 108-112, 164-168, 282-286, 316-320

**N-myristoylation sites:**

amino acids 34-40, 89-95, 215-221, 292-298, 293-299

489/615

**FIGURE 485**

AGAGTTCCTTTTTCTAGGTCGATTAGGTTATACATTGTTGAAGTATAGTTTCGAGTTAGAATT  
GGTCATTTTATTTTCAGTGTTTCACAGAAATCGAAGAAGACAGAAATGGCGCTTCTGTGGTGG  
ATATCTACAGTAGCAATACTGTTGTTTACTTCGACGATTTTGGGAACATACGTTGAAGCTGGT  
GCCGCTAAGTCTAACGAAGAAGAGATTGTGAACAAAAGCGAATTTGGAAGATTTCCACGAGGG  
TCGAGAAAGGATGCATCGGGGTGCCACAAGCCGGGCTACCCTGTACCCCTCATTCTCGCTGC  
CCTCCACCTCCCCATGTGCAGCGTCCTCGTCCTATTCTGCATGCTTAGTCTAACACCATCAGG  
CTCGTTTATCTTTTCTGTCATTGATCTCACCAGGAGCAAATCACTAGTGCGTGCTTCTGATTC  
ACGTAACGTAGTATGTAAATAAATGTCAGTGATATTATGAATTGGTAAACATTTCTGTTATC  
TAAATAAACAGTGAAGTTTGTGTGACTAAAAAA



490/615

**FIGURE 486**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96855
><subunit 1 of 1, 84 aa, 1 stop
><MW: 9274, pI: 9.70, NX(S/T): 1
MALLWWISTVAILLFTSTILGTVEAGAAKSNEEEIVNKSEFGRFPRGSRKDASGCHKPG
YPVPPHSRCPPPPHVQRPRPILHA
```

**Signal peptide:**

Amino acids 1-21

**N-glycosylation site:**

Amino acids 38-42

**N-myristoylation site:**

Amino acids 27-33

491/615

**FIGURE 487**

CGGGGACGGAAGCGGCCCCCTGGGCCCCGAGGGGCTGGAGCCGGGCCGGGGCG**ATGT**GGAGCGCG  
GGCCGCGGCGGGGCTGCCTGGCCGGTGCTGTTGGGGCTGCTGCTGGCGCTGTTAGTGCCGGGC  
GGTGGTGCCGCCAAGACCGGTGCGGAGCTCGTGACCTGCGGGTCGGTGCTGAAGCTGCTCAAT  
ACGCACCACCGCGTGCGGCTGCACTCGCACGACATCAAATACGGATCCGGCAGCGGCCAGCAA  
TCGGTGACCGGCGTAGAGGCGTCGGACGACGCCAATAGCTACTGGCGGATCCGCGGCGGCTCG  
GAGGGCGGGTGCCCGCGCGGGTCCCCGGTGCGCTGCGGGCAGGCGGTGAGGCTCACGCATGTG  
CTTACGGGCAAGAACCTGCACACGCACCACTTCCCGTCGCCGCTGTCCAACAACCAGGAGGTG  
AGTGCCTTTGGGGAAGACGGCGAGGGCGACGACCTGGACCTATGGACAGTGCGCTGCTCTGGA  
CAGCACTGGGAGCGTGAGGCTGCTGTGCGCTTCCAGCATGTGGGCACCTCTGTGTTCTGTCA  
GTCACGGGTGAGCAGTATGGAAGCCCCATCCGTGGGCAGCATGAGGTCCACGGCATGCCCAGT  
GCCAACACGCACAATACGTGGAAGGCCATGGAAGGCATCTTCATCAAGCCTAGTGTGGAGCCC  
TCTGCAGGTCACGATGAACTC**TGA**GTGTGTGGATGGATGGGTGGATGGAGGGTGGCAGGTGGG  
GCGTCTGCAGGGCCACTCTTGGCAGAGACTTTGGGTTTGTAGGGGTCTCAAGTGCCTTTGTG  
ATTAAAGAATGTTGGTCTATGAAA

492/615

**FIGURE 488**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96857
><subunit 1 of 1, 221 aa, 1 stop
><MW: 23598, pI: 6.96, NX(S/T): 0
MWSAGRGGAAWPVLLGLLLALLVPGGGAAGTGAELVTCGSVLKLLNTHHRVRLHSHDIKYGSG
SGQQSVTGVEASDDANSYWRIRGGSEGGCPRGSPVRCGQAVRLTHVLTGKNLHTHHFPSPLSN
NQEVSAFGEDGEGDDLDLWTVRCSGQHWEREAAVRFQHVGTSVFLSVTGEQYGSPIRGQHEVH
GMPSANTHNTWKAMEGIFIKPSVEPSAGHDEL
```

**Important features of the protein:****Signal peptide:**

amino acids 1-28

**Glycosaminoglycan attachment site.**

amino acids 62-66

**N-myristoylation sites.**amino acids 16-22, 25-31, 27-33, 61-67, 71-77, 86-92, 87-93,  
91-97, 190-196**Endoplasmic reticulum targeting sequence.**

amino acids 218-223

493/615

**FIGURE 489**

CAGCAGCCGAGACAGCAGCTGAGACGGCAGCGGCAGCTTCTCAGGGCCGGAGCCAGTTCTTGGAGGAGACTCTGC  
ACAGGGCATGGATCACTGTGGTGCCCTTTTCTGTGCTGTGCTTCTGACTTGCAGAATGCAACAACAGAGAC  
ATGGGAAGAACTCCTGAGCTACATGGAGAATATGCAGGTGTCCAGGGGCCGGAGCTCAGTTTTTCTCTCGTCA  
ACTCCACCAGCTGGAGCAGATGCTACTGAACACCAGCTTCCCAGGCTACAACCTGACCTTGACAGACACCCACCAT  
CCAGTCTCTGGCCTTCAAGCTGAGCTGTGACTTCTCTGGCCTCTCGCTGACCAGTGCCACTCTGAAGCGGGTGCC  
CCAGGCAGGAGGTGAGCATGCCCGGGGTGAGCAGGCCATGCAGTTCCCGCCGAGCTGACCCGGGACGCCTGCAA  
GACCCGCCCCAGGGAGCTGCGGCTCATCTGTATCTACTTCTCCAACACCCACTTTTTCAAGGATGAAACAACCTC  
ATCTCTGCTGAATAACTACGTCTGGGGGCCAGCTGAGTCATGGGCACGTGAACAACCTCAGGGATCCTGTGAA  
CATCAGCTTCTGGCACAACCAAAGCCTGGAAGGCTACACCCTGACCTGTGTCTTCTGGAAGGAGGGAGCCAGGAA  
ACAGCCCTGGGGGGGCTGGAGCCCTGAGGGCTGTCTACAGAGCAGCCCTCCCACTCTCAGGTGCTGTGCCGCTG  
CAACCACCTCACCTACTTTGCTGTTCTCATGCAACTCTCCCAGCCCTGGTCCCTGCAGAGTTGCTGGCACCTCT  
TACGTACATCTCCCTCGTGGGCTGCAGCATCTCCATCGTGGCCTCGCTGATCAGAGTCTGCTGCACCTTCCATTT  
CAGGAAGCAGAGTGACTCCTTAACACGTATCCACATGAACCTGCATGCCCTCCGTGCTGCTCCTGAACATCGCCTT  
CCTGCTGAGCCCCGATTGCAATGTCTCCTGTGCCCGGGTCAAGCATGCACGGCTCTGGCCGCTGCCCTGCACTA  
CGCGCTGCTCAGCTGCCTCACCTGGATGGCCATCGAGGGCTTCAACCTCTACCTCCTCCTCGGGCGTGTCTACAA  
CATCTACATCCGCAGATATGTGTCAAGCTTGGTGTGCTAGGCTGGGGGGCCCCAGCCCTCCTGGTGTGCTTTT  
CCTCTCTGTCAAGAGCTCGGTATACGGACCCTGCACAATCCCCGTCTTCGACAGCTGGGAGAATGGCACAGGCTT  
CCAGAACATGTCCATATGCTGGGTGCGGAGCCCCGTGGTGCACAGTGTCTGGTGCATGGGCTACGGCGGCCTCAC  
GTCCCTCTTCAACCTGGTGGTGTGCTGGCCTGGGCGCTGTGGACCCTGCGCAGGCTGCGGGAGCGGGCGGATGCACC  
AAGTGTGAGGGCCTGCCATGACACTGTCACTGTGCTGGGCCTCACCGTGTGCTGCTGGGAACCACTGGGCCTTGGC  
CTTCTTTTCTTTTGGCGTCTTCTGCTGCCCCAGCTGTTCTCTTACCATCTTAAACTCGCTGTACGGTTTCTT  
CCTTTTCTGTGTTCTGCTCCAGCGGTGCCGTGAGGCTGGAATCCTCAGCCTCTCTGGCCGCGAGTAGCCTGAGGCT  
CTCCCAACAACACAGTAGTCCGGGGCTCCTGGCCTGGAATCCTCAGCCTCTCTGGCCGCGAGTAGCCTGAGGCT  
ACGGCTCCTGCTAGAGAGGGTGGCAGGCCTGCTGCTGGACCCAGAGGCCACTGTGACCGCCAAGGGGCTTTTTC  
CACTTCCACGGCCTCTCCAGGCACTGAGGGGAAGGCATTGCTCTACCTCTCCCTGACATTTTGTCCGGGGCAGA  
TCCAACCTTACCTGGGGCAGCAAACCTTTGTCTGGTACCTGGGCCCAGCTCGCCAGGGATGTGGGCAGAGCACC  
GCCTGGGCATCAGGAAGCCAAGTTTCAAGGACTGTCTTTGAGTCTGTCTGTATGACCTTGGGCCTGCCACTTCTC  
ACAGACCCTAGGTATCCACAGCTGTGACATGGGGGCAAGCAGCTTTGTTTACGCCTAACCCAGGAGCTTAGTAAA  
AATTGCATAAGACCAGGGGGAAGAGTGTACAGCTGGGGTGGGAATTCCCGCGGCCTCCACCTGCTTGTAGGGGC  
AGGATCTCATTACAGGCTGCCCTGGAAGCACCTGCTTGGCCCTGCCACCTTCTCCAGGGGAGGGCCAGATGGCAT  
CCTGGCTTGGGGCGGGTGGGACCTACCCAGGCTCTGAGACTTTACTGGCCTATGCCTGAGGCCTCTTTTCTTTTA  
ACTCCCTAAATTATGATGACTCCAAGTCCAAGCCCACCCTTCCCAAAGATTGGGAGGTTCCGCCGTTCACAGAGG  
CTCCTCCTGCGGTGCTCCCAAGACTTCCATAGACCATCTGGACCAGTAGCCCATCCCGCAGTTTCTTGGGGGCA  
GAGGAAAACGCTTCTTTCTCCTCCAGCTGAATCAGCTGGATCCCAGTGTCTGGCTGTTTGGTGATTGGGCAAGA  
TTGAATTTGCCCAGGTAGGCGTGAGAGTGTGGGTTTTAAATTCGAAGCTCAGGCCATAGTTTCAAGAAATCACCC  
TTACCCACAGACCTTCATGAGACAGTGTCTCATGAAGCCAGTGCGTTTCCAGAACGAACACTAGGCGGCACCGTTG  
GTCCACACTCAGAGGCCCTTGGCGCCAAGACTGCATCTAGAATCGCTCAAACACCTGTTTGCAGACCCCATGCAC  
CAGCTGGAGGGGCGTAACCTGCAGGACTGCGCCTACTGAGTGACCAATTTCTCCAGGAGGAAAGGCAAGACAG  
CTTACACGGCCATTGTCTCTTTTCCCAATGCGGCGGTGCACTTTCGCTCTTGGGGGCTGCACCCAGACATAGC  
TGGCACCAGAGCAGGGTGTCTCAGGTGGTGGGTGCTCAGGGCCCTGCCCCAGGCCACTGGGCCGTTTTGATGACCT  
CAAAGGTACAGGCAGAAAATAGGAGCAGGATTTCCCTGGGGAAAAGTTATCCTGGGACATCTTCTGCTCTTCT  
GTACATTTCTAGATGCAAATAACTCCTTACCAGGCAGTGAGTGGCGTAGGCTCTGGAGCCAGGCTGCCTGGGCT  
CCAATGCCAGCTCTGCCACTTGCTAGCTGTGAGACTGTGGACAAACCACTCAGCCTCTGTGTGCCCTCAGTTTTCC  
TATTTGTAATAATAGAGACCATAGTGGTACCTATTTTGAAGACTAAGTAAAGAATTCAAATAAGAGACTTGGCA  
CAGAGTAAGTGCTCAGTAAAAA

494/615

**FIGURE 490**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96860
><subunit 1 of 1, 528 aa, 1 stop
><MW: 59000, pI: 8.73, NX(S/T): 9
MDHCGALFLCLCLLTQLQATTETWEELLSYMENMQVSRGRSSVFSSRQLHQLEQMLLNTS
FPGYNLTQTPTIQSLAFKLSCDFSGLSLTSATLKRVPQAGGQHARGQHAMQFPAELTRD
ACKTRPRELRLICIYFSNTHFFKDENNSSLNNYVLGAQLSHGHVNNLRDPVNISFWHNQ
SLEGYTLTCVFWKEGARKQPWGGWSPEGCRTEQPSHSQVLCRCNHLTYFAVLMQLSPALV
PAELLAPLTYISLVGCSISIVASLITVLLHFHFRKQSDSLTRIHMNLHASVLLLNI AFLL
SPAFAMSPVPGSACTALAAALHYALLSCLTWMAIEGFNLYLLLGRVYNIYIRRYVFKLGV
LGWGAPALLVLLSLSVKSSVYGPCPTIPVFDWENGTFQNM SICWVRSPVH SVLVMGYG
GLTSLFNLVVLAWALWTLRRLRERADAPSVRACHDTVTVLGLTVLLGTTWALAFFSFGVF
LLPQLFLFTILNSLYGFFLFWFCSQRCRSEAEAKAQIEAFSSSQTTQ
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-21

**Transmembrane domains:**

Amino acids 244-264;290-309;316-344;358-376;411-431;468-491

**N-glycosylation sites:**Amino acids 18-22;58-62;65-69;146-150;147-151;173-177;  
179-183;394-398;400-404**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 274-278

**N-myristoylation sites:**86 GLSLTS  
101 GGQHAR  
157 GAQLSH  
255 GCSISI  
311 GSACTA  
420 GGLTSL  
467 GTTWAL**Prokaryotic membrane lipoprotein lipid attachment sites:**

Amino acids 246-257;318-329

**Eukaryotic thiol (cysteine) proteases histidine active site:**

Amino acids 410-421

**G-protein coupled receptors family 2 proteins:**

Amino acids 273-302;314-343

495/615

**FIGURE 491**

CTTGGCTGCCCCGACAACAAGCTCGCCACCTGCGCTGGGCGCATCCACCATCCAAGGCCAGCT  
GAGGGGCACCAGACAGAGGATGAGGAGAGAGAGTGCACACGGGCTGCCCTGAGAGACATTTT  
CATGGACATCCTCATGCTGCTTCTGCTTTTGTGTGTAATATATGGGAGATTTTCCCAAGATGA  
ATACTCCCTCAATCAAGCTATCCGAAAGAATTTACAAGAAATGCCAGAACTGCTTGGGTGG  
CCTGAGAAACATCGCTGACTGGTGGGACTGGAGTCTGACCACACTTCTGGATGGCCTGTACCC  
GGGAGGCACCCCGTCAGCCCGTGCCGGGGGCTCAGCCTGGAGCTCTTGGAGGAAAATGCTA  
CCTAATAGGCAGTTCCGTAATTAGGCAGCTAAAAGTTTTTCTAGGCATTTATGCAAGCCTCC  
CAGGCCATTTTTCAGCACTCATCGAAGACTCTATTCTACATGTAGTCCCGAAGTTGGAGGCC  
TGAGAACCCCTACCTGATAGACCCAGAGAACCAAAACGTGACCCTGAATGGTCCTGGGGGCTG  
TGGGACAAGGGAGGACTGTGTGCTCAGCCTGGGCAGAACAAAGGACTGAAGCCACACAGCCCT  
GTCCCGACTCAGGGCCAGCATGTGGATTGACCGCAGCACCAGGGCTGTGTCTGTGCACTTCAC  
TCTCTATAACCCTCCAACCCAACTCTTCACCAGCGTGTCCCTGAGAGTGGAGATCCTCCCTAC  
GGGGAGTCTCGTCCCTCATCCCTGGTGGAGTCATTGAGCATCTTCCGCAGCGACTCAGCCCT  
GCAGTACCACCTCATGCTTCCCCAGCTGGTCTTCTGCACTCAGCCTGATCCACCTCTGTGT  
TCAACTCTACCGTATGATGGACAAGGGCGTCTCAGCTACTGGCGAAAGCCAAGGAAGTGGCT  
GGAGGTAGCCTCTCTTGTGTCAATTTCTTTTGAAAAATAACAATAAACTGTTTATATCTTGAA  
AAAATAATTTAAATAAGAAATTGATTATGCACTAGCTACTGCCAACATTATTGCAGTTTTCTC  
CCTCTGTAGTGTTAATCTCAAAACAGCATTTGAGATCAGGTATCATTTAGTGTTGTTACAGTT  
ACCGTCATGTACCACACGAATTTAGCCAAGGTGGTGGTCCCATAGATCATATGGTGCTAAG  
AAATTTCTGTACCTAATGACATCTTGATTCTGACCTTGATGTAGGCCTAGGCTAAATATGT  
CTGTTTGTATCTTAGCTTTTAATAAAGAAGTTTAAAAATAAAAA

496/615

**FIGURE 492**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96861
><subunit 1 of 1, 300 aa, 1 stop
><MW: 33649, pI: 9.26, NX(S/T): 1
MRRESRTRAALRDISMDILMLLLLLLCVIYGRFSQDEYSLNQAIRKEFTRNARNCLGGLRN
IADWWDWSLTLLDGLYPGGTPSARVPGAQPGALGGKCYLIGSSVIRQLKVFPRHLCKPP
RPFSAIEDSIPTCSPEVGGPENPYLIDPENQNVTLNGPGGCGTREDCVLSLGRTRTEAH
TALSRLRASMWIDRSTRAVSVHFTLYNPPTQLFTSVSLRVEILPTGSLVPSSLVESFSIF
RSDSALQYHMLPQLVFLALSLIHLVCVQLYRMMMDKGVLSYWRKPRNWLEVASLVSFSEK
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-30

**Transmembrane domain:**

Amino acids 250-267

**N-glycosylation site:**

Amino acids 153-157

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 2-6

**N-myristoylation sites:**

Amino acids 56-62;75-81;79-85;80-86;88-94;92-98;160-166

497/615

**FIGURE 493**

TCTCAGGGCTTCATACAGGAAATCTATTGCTGTGTCAAGTTCAGAGAAAAGCTTCTGTTTCGT  
CCAAGTTACTAACCAGGCTAAACCACATAGACGTGAAGGAAGGGGCTAGAAGGAAGGGAGTGC  
CCCCTGTTGATGGGGTAAGAGGATCCTGTACTGAGAAGTTGACCAGAGAGGGTCTCACCATG  
CGCACAGTTCCTTCTGTACCTGTGTGGAGGAAAAGTACTGAGTGAAGGGCAGAAAAAGAGAAA  
ACAGAAATGCTCTGCCCTTGGAGAAGTCTAACCTAGGGCTACTGTTGATTTTGACTATCTTC  
TTAGTGGCCGAAGCGGAGGGTGTGCTCAACCAAACAACCTATTAATGCTGCAAACCTAGCAAG  
GAGAATCATGCTTTAGCTTCAAGCAGTTTATGTATGGATGAAAAACAGATTACACAGAACTAC  
TCGAAAGTACTCGCAGAAGTTAACACTTCATGGCCTGTAAAGATGGCTACAAATGCTGTGCTT  
TGTTGCCCTCCTATCGCATTAAAGAAATTTGATCATAATAACATGGGAAATAATCCTGAGAGGC  
CAGCCTTCCTGCACAAAAGCCTACAGGAAAGAAACAAATGAGACCAAGGAAACCAACTGTACT  
GATGAGAGAATAACCTGGGTCTCCAGACCTGATCAGAATTTCGGACCTTCAGATTCGTCCAGTG  
GCCATCACTCATGACGGGTATTACAGATGCATAATGGTAACACCTGATGGGAATTTCCATCGT  
GGATATCACCTCCAAGTGTTAGTTACACCTGAACTGACCCTGTTTCAAACAGGAATAGAACT  
GCAGTATGCAAGGCAGTTGCAGGGAAGCCAGCTGCGCAGATCTCCTGGATCCCAGAGGGCGAT  
TGTGCCACTAAGCAAGAATACTGGAGCAATGGCACAGTGAAGTGTAAAGAGTACATGCCACTGG  
GAGGTCCACAATGTGTCTACCGTGACCTGCCACGTCTCCCATTTGACTGGCAACAAGAGTCTG  
TACATAGAGCTACTTCCTGTTCCAGGTGCCAAAAAATCAGCAAAATTATATATTCCATATATC  
ATCCTTACTATTATTATTTTGACCATCGTGGGATTCATTTGGTTGTTGAAAGTCAATGGCTGC  
AGAAAATATAAATTGAATAAAACAGAATCTACTCCAGTTGTTGAGGAGGATGAAATGCAGCCC  
TATGCCAGCTACACAGAGAAGAACAATCCTCTCTATGATACTACAAACAAGGTGAAGGCATCT  
CAGGCATTACAAAGTGAAGTTGACACAGACCTCCATACTTTATAAGTTGTTGGACTCTAGTAC  
CAAGAAACAACAACAACGAGATACATTATAATTACTGTCTGATTTTCTTACAGTTCTAGAAT  
GAAGACTTATATTGAAATTAGGTTTTCCAAGGTTCTTAGAAGACATTTTAAATGGATTCTCATT  
CATACCCTTGTATAATTGGAATTTTTGATTCTTAGCTGCTACCAGCTAGTTCTCTGAAGAACT  
GATGTTATTACAAAGAAAATACATGCCCATGACCAAATATTCAAATTGTGCAGGACAGTAAAT  
AATGAAAACCAAATTTCCCTCAAGAAATAACTGAAGAAGGAGCAAGTGTGAACAGTTTCTTGTG  
TATCCTTTTCAAGAAATTTTTAATGTACATATGACATGTGTATATGCCTATGGTATATGTGTCAA  
TTTATGTGTCCCCTTACATATACATGCACATATCTTTGTCAAGGCACCAGTGGGAACAATACA  
CTGCATTACTGTTCTATACATATGAAAACCTAATAATATAAGTCTTAGAGATCATTTTATATC  
ATGACAAGTAGAGCTACCTCATTCTTTTTAATGGTTATATAAAATTCATTGTATAGTTATAT  
CATTATTTAATTAATAAACAACCCTAATGATGGATATTTAGATTCTTTAAGTTTTGTTTATTT  
CTTTTAAGTTTTGTTTGTGTTATAAACAATACCACATAGAATGTTTCTTGTTCATATATCTCT  
TTGTTTTTGTAGTATATCTGTAGGATAACTTTCTTGAGTGGAATTGTCAGGTCAAAGGGTTTGT  
GCATTTTACTATTGATATATATGTTAAATTGTGTCAAATATATATGTCAAATTCCTCCAACA  
TTGTTTAAATGTGCCTTTCCCTAAATTTCTATTTTAATAACTGTACTATTCCTGCTTCTACAG  
TTGCCACTTTCTCTTTTAAATCAACCAGATTAAATATGATGTGAGATTATAATAAGAATTATA  
CTATTTAATAAAAAATGGATTATATA



498/615

**FIGURE 494**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96866
><subunit 1 of 1, 348 aa, 1 stop
><MW: 39069, pI: 8.13; NX(S/T): 10
MLCPWRTANLGLLLILTIFLVAEAEAGAAQPNNSLMLQTSKENHALASSSLCMDEKQITQN
YSKVLAEVNTSWPVKMATNAVLCCPPIALRNLIITWEIILRGQPSC TKAYRKETNETKE
TNCTDERITWVSRPDQNSDLQIRPVAITHDGYRCIMVTPDGNFHRGYHLQVLVTPELTL
FQNRNRTAVCKAVAGKPAAQISWIPEGDCATKQEYWSNGTVTVKSTCHWEVHNVSTVTC
VSHLTGNKSLYIELLPVPGAKKS AKLYIPYIIITIIITIVGFIWLLKVN GCRKYKLNKT
ESTPVVEEDEMOPYASYTEKNNPLYDTTNKVKASQALQSEVDTDLHTL
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-24

**Transmembrane domains:**

Amino acids 78-98;267-286

**N-glycosylation sites:**Amino acids 31-35;60-64;69-73;116-120;122-126;185-189;  
218-222;233-237;247-251;298-302**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 112-116

**N-myristoylation sites:**

Amino acids 103-109;259-265

499/615

**FIGURE 495**

CCAGGTGCACAGCGCATCGCCCCGAGGCTGTCACCGCCCTGCCCGCCACCCAGCTGTCCTG  
GACCCAGGGGAGGGAGAGGCTGGACGCCAGGTGCGCGGACACAGAAGCGTCTAAGCACAGCT  
TCCTCCTTGCCGCTCCGGGAAGTGGGCAGCCAGCCAGGAACCAGTACCACCTGCACCATGGG  
GCTGTCCCGGAAGGAGCAGGTCTTCTTGCCCTGCTGGGGGCTCGGGGGTCTCAGGCCTCAC  
GGCACTCATTCTCCTCCTGGTGGAGGCCACCAGCGTGCTCCTGCCACAGACATCAAGTTTGG  
GATCGTGTGTTGATGCGGGCTCCTCCACACGTCCCTCTTCTGTATCAGTGGCCGGCGAACAA  
GGAGAATGGCACGGGTGTGGTCAGCCAGGCCCTGGCCTGCCAGGTGGAAGGGCCTGGAATCTC  
CTCCTACACTTCTAATGCTGCACAGGCTGGTGAGAGCCTGCAGGGCTGCTTGGAGGAGGCGCT  
GGTGCTGATCCAGAGGCCAGCATCGGAAAACACCCACGTTCTGGGGGCCACGGCTGGCAT  
GAGGTTGCTCAGCCGGAAGAACAGCTCTCAGGCCAGGGACATCTTGCAGCAGTACCCAGGT  
CCTGGGGCGGTCTCCCGTGGACTTTTGGGGTGCCGAGCTCCTGGCGGGCAGGCCAGGTGC  
CTTTGGTTGGATCACTGTCAACTACGGCTTGGGGACGCTGGTCAAGTACTCCTTCACTGGAGA  
ATGGATCCAGCCTCCGGAGGAGATGCTGGTGGGTGCCCTGGACATGGGAGGGCCTCCACCCA  
GATCACGTTCTGCTGCTGGGGGCCCCATCTTGGACAAGAGCACCCAGGCCGATTTTTCGCTCTA  
CGGCTCCGACTACAGCGTCTACACTCACAGCTACCTGTGCTTTGGACGGGACCAGATGCTGAG  
CAGGCTCCTCGTGGGGCTGGTGAGAGCCGCCCGGCTGCCCTGCTCCGTCACCCGTGCTACCT  
CAGCGGCTACCAGACCACACTGGCCCTGGGCCGCTGTATGAGTACCCCTGTGTCCACGCCAC  
GCCCCGCTGAGCCTCCCCCAGAACCTCACAGTTGAAGGGACAGGCAACCCTGGAGCCTGCGT  
CTCAGCCATCCGGGAACTTTTCAACTTCTCCAGCTGCCAGGGCCAGGAGGACTGCGCTTTGA  
CGGGGTCTACCAGCCCCCGCTGCGGGGCCAGTTCTATGTGGAGGCCAGCTACCCTGGGCAGGA  
CCGCTGGCTGCGGGACTACTGTGCCTCAGGCCTGTACATCCTCACCCCTCCTGCACGAGGGCTAC  
GGGTTTCAGCGAGGAGACCTGGCCCAGCCTCGAGTTCCGAAAGCAGGCGGGCGGTGTGGACATT  
GGCTGGACACTGGGCTACATGCTGAACCTGACCGGGATGATCCCGGCCGATGCGCCGGCTCAG  
TGGCGGGCAGAGAGCTACGGCGTCTGGGTGGCCAAAGTGGTGTTCATGGTGCTGGCCCTGGTG  
GCGGTGGTGGGGGCTGCCTTGGTCCAGCTCTTCTGGTTGCAGGACTAGTGGGAAGGCGGAGGT  
GGGCCCCCACAGAGCCCACAGGCAGCTGCGTCCCGGATGCTGGAGGCTTCTGAGCCCTGAGC  
GCCGTGGGGCCTTGCTCTGTGGCTCTGCCACGGTCAGGTGACAGCCACCTCCAGGGCACCGT  
CAGGGTGGTGCTGGCCACAGAGGCTGCATGACCTCCCTCCCGGCGTCCCTCCCCAACCTCC  
TTCCGCAACTGGGCTTCCAGGGCCGTAGGTGCCTTTCTGCACACAGGCCGCCAGGACTCGTGG  
TGTCTCCAGGCTGTGTGACTGCAGGGCCACATGCTGCCTGCAAACAGGGCAAGACCACGGAGG  
CACAGGGGTCCTGCTCCTGATGGGGCCTCAGGAGGGGCGGAGAGGGGTGGAAGGGAGGGAGCT  
GCCCCACCTGGACCCCCGCTCTCCCTGCTGTTGTCTGAGCAGATGGATGGAGTCCAGGCCTGG  
GGGCTTCTGCTGGGCCAGCCCGCCTCCACACCCACTTGGAGGGTGAGACTGCAGTGGGGGT  
TGTTTTTATTAAAAGCATCATGGACACAGCAAAAAAAAAAAAAAAAAA

500/615

**FIGURE 496**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96870
><subunit 1 of 1, 458 aa, 1 stop
><MW: 49377, pI: 4.98, NX(S/T): 5
MGLSRKEQVFLALLGASGVSGLTALILLVEATSVLLPTDIKFGIVFDAGSSHTSLFLYQ
WPANKENGTVVVSQALACQVEGPGISSYTSNAAQAGESLQGCLEEALVLIPEAQHRKTPT
FLGATAGMRLLSRKNSSQARDIFAAVTQVLGRSPVDFWGAELLAGQAEGAFGWITVNYGL
GTLVKYSFTGEWIQPPPEMLVGALDMGGASTQITFVPGGPILDKSTQADFRLYGSDYSVY
THSYLCFGRDQMLSRLLVGLVQSRPAALLRHPCYLSGYQTTALGPLYESPCVHATPPLS
LPQNLTVEGTGNGACVSAIRELFNFSSCQGOEDCAFDGVYQPPLRGQFYVEASYPGQDR
WLRDYCASGLYIILTLLHEGYGFSEETWPSLEFRKQAGGVDIGWTLGYMLNLTGMI PADAP
AQWRAESYGVWVAKVVFVVLALVAVVGAALVQLFWLQD
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-21

**Transmembrane domain:**

Amino acids 428-449

**N-glycosylation sites:**

Amino acids 67-71;135-139;304-308;325-329;410-414

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 133-137

**N-myristoylation sites:**Amino acids 50-56;123-127;165-171;207-213;234-240;  
259-265;311-317;314-320;331-337;398-404;  
413-419;429-435**GDA1/CD39 family of nucleoside phosphatases proteins:**

Amino acids 43-59;202-215

501/615

**FIGURE 497**

GCCTTATAAAGTAGCCTCTGCATCTGCCTGCCTCGGGCAGAGGAGGGCTACCCTGGGGCTGAG  
AGTTCACCTGTCTCAGGAACCACCTGAGCCACAGATCCTGTGGGCAGCGGCCAGGGCAGCCA  
**TGG**CCTGGGCAAGTAGGCTGGGCCTGCTGCTGGCACTGCTGCTGCCCCGTGGTTCGGTGCCTCCA  
CGCCAGGCACCGTGGTCCGACTCAACAAGGCAGCATTGAGCTACGTGTCTGAAATTGGGAAAG  
CCCCCTCTCCAGCGGGCCCTGCAGGTCACTGTCCCTCATTTCTGGACTGGAGTGGAGAGGCGC  
TTCAGCCCACCAGGATCCGGATTCTGAATGTCCATGTGCCCCGCTCCACCTGAAATTCATTG  
CTGGTTTCGGAGTGCCTGCTGGCAGCAGCTAATTTTACTTTCAAGGTCTTTCGCGCCCCAG  
AGCCCCCTGGAGCTGACGCTGCCTGTGGAAGTGTGGCTGACACCCGCGTGACCCAGAGCTCCA  
TCAGGACCCCTGTGGTCAGCATCTCTGCCTGCTCTTTATTCTCGGGCCACGCCAACGAGTTTG  
ATGGCAGTAACAGCACCTCCCACGCGCTGCTGGTCTGGTGCAGAAGCACATTAAAGCTGTCT  
TGAGTAACAAGCTGTGCTGAGCATCTCCAACCTGGTGCAGGGTGTCAATGTCCACCTGGGCA  
CCTTAATTGGCCTCAACCCCGTGGGTCTGAGTCCCAGATCCGCTATTCCATGGTCAGTGTGC  
CCACTGTCAACAGTGAATACTTTCCCTGGAAGTCAATGCTGTTCTCTTCTGCTGGGCAACC  
CCATCATCTCTGCCACGGATGCCACCCCTTTTGTGTTGCCAAGGCATGTGGGTACCGAGGGCT  
CCATGGCCACCGTGGGCCTCTCCAGCAGCTGTTTGACTCTGCGCTCCTGCTGCTGCAGAAGG  
CCGGTGCCCTCAACCTGGACATCACAGGGCAGCTGAGGTTCGGATGACAACCTGCTGAACACCT  
CTGCTCTGGGCCGGCTCATCCCGGAGGTGGCCCGCCAGTTTCCCGAGCCCATGCCTGTGGTGC  
TCAAGGTGCGGCTGGGTGCCACACCTGTGGCCATGCTCCACACAAACAACGCCACCCCTGCGGC  
TGCAGCCCTTCGTGGAGGTCCTGGCCACAGCCTCCAACCTCGGCTTTCAGTCCCTCTTCTCCC  
TGGATGTGGTAGTGAACCTGAGACTCCAGCTCTCTGTGTCCAAGGTGAAGCTTCAGGGGACCA  
CGTCTGTGCTGGGGGATGTCCAGCTCACGGTGGCCTCCTCCAACGTGGGCTTCATTGATACAGAT  
CAGGTGCGCACACTGATGGGCACCGTTTTTGTAGAAGCCCCTGCTGGACCATCTCAATGCTCTC  
TTGGCCATGGGAATTGCCCTCCCTGGTGTGGTCAACCTCCACTATGTTGCCCTTGAGATCTTT  
GTCTATGAGGGCTACGTGGTGATATCCAGTGGACTCTTCTACCAGAGCT**TGAGG**CAAGACCACT  
GGGAGGCCTGAGAGTGGGCCAGCTCGCTGCTCAGGCGAATTTCTCATTTCAAGCCACTGGGGA  
AACTGAGGCAAAACCATACTTAGTCATCACCAACAAGCTGGACTGCTTAGCTGGGCTGTTTTA  
TCTTCCCTGAGTGCCTGGGTCTCCCTCCCTCACTTCTGCCCTTTCCTTCCCTCCTCCTCTTCT  
CCTCCCTCTTCCCTCATCTCCCCCTCCTTCTGCCCCACCCCAGGGGGGAGCAGACTGCT  
CCTCCAGGCTGTATAGACCTGCCCTCTTGCAATTAACAACCTTCTCTTGAGCTGC

502/615

**FIGURE 498**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96872
><subunit 1 of 1, 458 aa, 1 stop
><MW: 49158, pI: 8.72, NX(S/T): 4
MAWASRLGLLLALLLPVVGASTPGTVVRLNKAALSYVSEIGKAPLQRALQVTVPHFLLDWS
GEALQPTRIRILNVHVPRLHLKFIAGFGVRLAAANFTFKVFRAPEPLELTLPVELLADT
RVTQSSIRTPVVSISACSLFSGHANEFDGSNSTSHALLVLVQKHIAVLNKLCLSSISNL
VQGVNVHLGTLIGLNPVGPESQIRYSMVSVPTVTSYISLEVNAVLFLLGNPIILPTDAT
PFVLPRHVGTEGSMATVGLSQQLFDSALLLLQKAGALNLDITGQLRSDDNLLNTSALGRL
IPEVARQFPEPMPVVLKVRLGATPVAMLHTNNATLRLQPFVEVLATASNSAFQSLFSLDV
VNNLRLQLSVSKVKLQGTTSVLGDVQLTVASSNVGFIDTDQVRTLMGTVFEEKPLLDHLNA
LLAMGIALPGVVNLHYVAPEIFVYEGYVVISSGLFYQS
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-20

**Transmembrane domain:**

Amino acids 217-236

**N-glycosylation sites:**

Amino acids 96-100;151-155;293-297;332-336

**N-myristoylation sites:**

Amino acids 8-14;149-155;189-195;249-255;252-258;283-289

**LBP / BPI / CETP family proteins:**

Amino acids 22-50; 251-287

503/615

**FIGURE 499**

TTGAAAATCTACTCTATCAGCTGCTGTGGTTGCCACCATTCTCAGGACCCTCGCC**ATG**GAAAGC  
CCTTATGCTGCTCACCCTGTCTGTTCTGCTCTGCTGGGTCTCAGCTGACATTCGCTGTCACTC  
CTGCTACAAGGTCCCTGTGCTGGGCTGTGTGGACCGGCAGTCCTGCCGCCTGGAGCCAGGACA  
GCAATGCCTGACAACACATGCATACCTTGGTAAGATGTGGGTTTTCTCCAATCTGCGCTGTGG  
CACACCAGAAGAGCCCTGTCAGGAGGCCTTCAACCA~~AA~~ACCAACCGCAAGCTGGGTCTGACATA  
TAACACCACCTGCTGCAACAAGGACAACCTGCAACAGCGCAGGACCCCGGCCCACTCCAGCCCT  
GGGCCTTGCTCTTCCTTACCTCCTTGGCTGGCCTTGGCCTCTGGCTGCTGCAC**TG**AGACTCATT  
CCATTGGCTGCCCCCTCCTCCCACCTGCCTTGGCCTGAGCCTCTCTCCCTGTGTCTCTGTATCC  
CCTGGCTTTACAGAATCGTCTCTCCCTAGCTCCCATTTCTTTAATTAAACACTGTTCCGAGTG  
GTCTCCTCATCCATCCTTCCCACCTCACACCCTTCACTCTCCTTTTTCTGGGTCCCTTCCCAC  
TTCCTTCCAGGACCTCCATTGGCTCCTAGAAGGGCTCCCCACTTTGCTTCTATACTCTGCTG  
TCCCCTACTTGAGGAGGGATTGGGATCTGGGCCTGAAATGGGGCTTCTGTGTTGTCCCCAGTG  
AAGGCTCCCACAAGGACCTGATGACCTCACTGTACAGAGCTGACTCCCCAAACCCAGGCTCCC  
ATATGTACCCCATCCCCATACTCACCTCTTCCATTTTGAGTAATAAATGTCTGAGTCTGGA  
AAAAAAAAAAAAAAAAAA

504/615

**FIGURE 500**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96878  
><subunit 1 of 1, 125 aa, 1 stop  
><MW: 13821, pI: 8.60, NX(S/T): 2  
MKALMLLTLSVLLCWVSADIRCHSCYKVPVLGCVDRQSCRLEPGQQCLTTHAYLGKMWVFSNL  
RCGTPEEPCQEAFNQTNRKLGITYNTTCCNKDNCNSAGPRPTPALGLVFLTSLAGLGLWLLH

**Important features of the protein:****Signal peptide:**

amino acids 1-18

**N-glycosylation sites.**

amino acids 77-81, 88-92

**N-myristoylation site.**

amino acids 84-90

**Ly-6 / u-PAR domain protein signature.**

amino acids 85-98

505/615

**FIGURE 501**

GGAGCCTCCTAATGCAGTCTTCTGCACAGTCCTGGGGACTGACTGACTGAATCACACCTCTGG  
GGCTGGGGGGCTGCTGAC**ATG**TGTGCCTTTCCTTGGCTGCTTCTTCTCCTGCTGCTCCAGGAGG  
GCAGCCAAAGGAGACTCTGGAGATGGTGTGGATCCGAGGAAGTGGTTGCGGTCCTTCAGGAGT  
CCATCAGCCTCCCCCTGGAAATACCACCAGATGAAGAGGTTGAGAACATCATCTGGTCCTCTCAC  
AAAAGTCTTGCCACTGTGGTGCCAGGGAAAGAGGGACATCCAGCTACCATCATGGTGACCAAT  
CCACACTACCAGGGCCAAGTGAGCTTCCTGGACCCAGCTATTCCTGCATATCAGCAATCTG  
AGCTGGGAGGATTGAGGGCTTTACCAAGCTCAAGTCAACCTGAGAACATCCCAGATCTCTACC  
ATGCAGCAGTACAATCTATGTGTCTACCATCCTAACTATGCTTCTGAGAAGCCTTCAACAGCC  
TTCTGCCTCCTGGCCAAGGGATTGCTCATCTTCTTGCTCTTGGTAATTCTGGCCATGGGACTC  
TGGGTCATCCGAGTCCAGAAAAGACACAAAATGCCAAGGATGAAGAACTCATGAGAAACAGA  
ATGAAATTGAGGAAGGAGGCAAAGCCTGGCTCCAGCCCTGCCT**TG**ACTGCTCCTTGGGAACCCC  
AGTCCTGAGCTTGGTTCCTCCCAGCACCCAGAGAATCCTTCCTCAGCTCTCTTCTTCCAGG  
GGAAGGAGGTGCTCAGGGGTGGGTATCCAGAGAGCCATACTTCTGAGGGAAGACTGGCTGGCA  
ATAAAGTCAAATTAAGTGACCACA



506/615

**FIGURE 502**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96879
><subunit 1 of 1, 198 aa, 1 stop
><MW: 22584, pI: 9.40, NX(S/T): 1
MCAFPWLLLLLLLLQEGSQRRLLWRWCGSEEVVAVLQESISLPLEIPPDEEVENIIWSSHKS
LATVVPKGKEGHPATIMVTNPHYQGQVSFLDPSYSLHISNLSWEDSGLYQAQVNLRTSQIS
TMQQYNLCVYHPNYASEKPSTAFCLLAKGLLI FLLLVLAMGLWVIRVQKRHKMPRMKKL
MRNRMKLRKEAKPGSSPA
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-18

**Transmembrane domain:**

Amino acids 144-165

**N-glycosylation site:**

Amino acids 99-103

**N-myristoylation site:**

Amino acids 106-112

507/615

**FIGURE 503**

ACGGGCCGCGAGCGGCAGTGACGTAGGGTTGGCGCACGGATCCGTTGCGGCTGCAGCTCTGCAG  
TCGGGCCGTTCCCTTCGCCGCCGCCAGGGGTAGCGGTGTAGCTGCGCAGCGTCGCGCGCGCTAC  
CGCACCCAGGTTTCGGCCCCGTAGGCGTCTGGCAGCCCCGGCGCCATCTTCATCGAGCGCC**ATGGC**  
CGCAGCCTGCGGGCCGGGAGCGGCCGGGTACTGCTTGCTCCTCGGCTTGCAATTTGTTTCTGCT  
GACCGCGGGCCCTGCCCTGGGCTGGAACGACCCTGACAGAATGTTGCTGCGGGATGTAAAAGC  
TCTTACCCTCCACTATGACCGCTATAACACCTCCCGCAGGCTGGATCCCATCCACAGTTGAA  
ATGTGTTGGAGGCACAGCTGGTTGTGATTCTTATACCCCAAAGTCATACAGTGTGAGAACAA  
AGGCTGGGATGGGTATGATGTACAGTGGGAATGTAAGACGGACTTAGATATTGCATACAAATT  
TGGAAAACCTGTGGTGAGCTGTGAAGGCTATGAGTCCTCTGAAGACCAGTATGTACTAAGAGG  
TTCTTGTGGCTTGGAGTATAATTTAGATTATACAGAACTTGGCCTGCAGAACTGAAGGAGTC  
TGGAAAGCAGCACGGCTTTGCCTCTTTCTCTGATTATTATTATAAGTGGTCCTCGGCGGATTC  
CTGTAACATGAGTGGATTGATTACCATCGTGGTACTCCTTGGGATCGCCTTTGTAGTCTATAA  
GCTGTTCTGAGTGACGGGCAGTATTCTCCTCCACCGTACTCTGAGTATCCTCCATTTTCCCA  
CCGTTACCAGAGATTCACCAACTCAGCAGGACCTCCTCCCCAGGCTTTAAGTCTGAGTTCAC  
AGGACCACAGAATACTGGCCATGGTGCAACTTCTGGTTTTGGCAGTGCTTTTACAGGACAACA  
AGGATATGAAAATTTCAGGACCAGGGTCTGGACAGGCTTGGGAACCTGGTGGAATACTAGGATA  
TTTGTTTTGGCAGCAATAGAGCGGCAACACCCTTCTCAGACTCGTGGTACTACCCGTCCTATCC  
TCCCTCCTACCCCTGGCACGTGGAATAGGGCTTACTCACCCCTTCATGGAGGCTCGGGCAGCTA  
TTCGGTATGTTCAAACCTCAGACACGAAAACCAGAACTGCATCAGGATATGGTGGTACCAGGAG  
ACGA**TAA**AGTAGAAAGTTGGAGTCAAACACTGGATGCAGAAATTTTGGATTTTTCATCACTTT  
CTCTTTTAGAAAAAAGTACTACCTGTTAACAATTGGGAAAAGGGGATATTCAAAAGTTCTGTG  
GTGTTATGTCCAGTGTAGCTTTTTGTATTCTATTATTTGAGGCTAAAAGTTGATGTGTGACAA  
ATACTTATGTGTTGTATGTCAGTGTAACATGCAGATGTATATTGCAGTTTTTGAAAGTGATC  
ATTACTGTGGAATGCTAAAAATACATTAATTTCTAAAACCTGTGATGCCCTAAGAAGCATTAA  
GAATGAAGGTGTTGTACTAATAGAACTAAGTACAGAAAATTTAGTTTTAGGTGGTTGTAGC  
TGATGAGTTATTACCTCATAGAGACTATAATATTCTATTTGGTATTATATTATTTGATGTTTG  
CTGTTCTTCAAACATTTAAATCAAGCTTTGGACTAATTATGCTAATTTGTGAGTTCTGATCAC  
TTTTGAGCTCTGAAGCTTTGAATCATTCAAGTGGTGGAGATGGCCTTCTGGTAACTGAATATTA  
CCTTCTGTAGGAAAAGGTGGAAAATAAGCATCTAGAAGGTTGTTGTGAATGACTCTGTGCTGG  
CAAAAATGCTTGAAACCTCTATATTTCTTTTCGTTTCATAAGAGGTAAAGGTCAAATTTTCAAC  
AAAAGTCTTTTAATAACAAAAGCATGCAGTTCTCTGTGAAATCTCAAATATTGTTGTAATAGT  
CTGTTTCAATCTTAAAAAGAATCA

508/615

**FIGURE 504**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96889  
><subunit 1 of 1, 339 aa, 1 stop  
><MW: 36975, pI: 7.85, NX(S/T): 1  
MAAACGPGAAGYCLLLGLHLFLLTAGPALGWNDPDRMLLRDVKALTLHYDRYTTSRRLDPIPO  
LKCVGGTAGCDSYTPKVIQCQNKGDGYDVQWECKTDLDIAYKFGKTVVSCEGYESSEDQYVL  
RGSCGLEYNLDYTELGQLKESGKQHGFAFSFYKSSADSCNMSGITIVVLLGIAFVV  
YKLFLSDGQYSPPPYSEYPPFSHRYQRFTNSAGPPPPGFKSEFTGPQNTGHGATSGFGSAFTG  
QQGYENSGPGFWTGLGTGGILGYLFGSNRAATPFSDSWYYPSYPPSYPGTWNRAYSPLHGGSG  
SYSVCSNSDTKTRTASGYGGTRRR

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 171-190

**N-glycosylation site.**

amino acids 172-176

**Glycosaminoglycan attachment sites.**

amino acids 244-248, 259-263, 331-335

**Tyrosine kinase phosphorylation site.**

amino acids 98-106

**N-myristoylation sites.**amino acids 68-74, 69-75, 131-137, 241-247, 247-253, 266-272,  
270-276, 278-284, 312-318

509/615

**FIGURE 505**

GCAAAAGGAAGGGAGGGAAGCACTCCATCATCTCACTGGGAAGAACGGCACGGGCATACCTGC  
AGCTACTGGGGTTCCACTGGGCTTGAGGGTCGATTTTTCACCTTTTGAAGGACAAG**ATG**CATT  
GGAAGATGTTGCTGCTTCTGCTGTTGTATTACAATGCTGAGGCTTCTATGTGCCACAGGTGGA  
GCAGGGCTGTGCTCTTCCCTGCCGCCCACCGGCCAAAGAGGTCTCATCACTGCCATTGAACC  
CAGTCCTGCAGACCTCCCTGGAGGAGGTGGAGCTGCTCTACGAGTTCCTGCTGGCCGAACCTTG  
AGATCAGCCCTGACCTGCAGATCTCCATCAAGGACGAGGAGCTGGCCTCCTTGCGGAAGGCCT  
CAGACTTCCGCACCGTCTGCAACAACGTCATCCCCAAGAGCATCCCAGACATCCGCCGGCTCA  
GCGCCAGCCTCTCCAGCCACCCTGGCATCCTCAAGAAAGAAGACTTTGAAAGGACAGTGCTGA  
CCCTGGCCTACACAGCCTACCGCACAGCCCTGTCCCACGGCCATCAGAAGGACATCTGGGCGC  
AGTCCCTCGTTAGCCTCTTCCAGGCCCTGAGGCACGACTTGATGCGCTCCTCACAGCCGGGAG  
TACCTCCCT**TGA**GAGACTGGCCACACCAGGACCTCAGAGCAGGGACCAGCACAGTAATCCAGA  
AAGTCTTCATTCTCTACTCCATTTACAGAGACCAGCAACAAAACACTTACCGCTGACACAGAG  
CAGCAGAGATCAAACAGTAACCCCGATGCTCTTTTCTCCTTGATGTTTCTGGAAGACACATC  
TGATTCATGCCATCATGTGACCTGGGCTGGAAGAAAGGGCTGGAATGGTCATTCAAGACGCCT  
CCATGGGCAGAATGGTTTGCCTATGGCAGGCAGAATTCTGATATGCTTCAACCCAGAGCAGTG  
GCCACACACTCAAGAGTGAGAACAGGCGTGAGCCACCGTGCCTGGCCAGGATCTAAAAACTT  
TCTAAGTTTCTCCATCGTTGGCATCCTCACAGCTATCTCCAATGTCACTCAAGAGACATCAA  
CAGACATTTAACTGCTGCAGACTTCATTGCTCTGTACCTCACCTTGAATCTAACAAATCAAA  
GTATTTCTGCAGGTCCAATGGTCTAAATCAAATGCTTGTTAAATGACTTTTTTACAACACCCCTT  
ACTTTCCTAATCCATTTCAATCTTATTTTTTTTTATTGTGGTAAAAAACACATCACGTAAATG  
TACCATCTTAACCATTTTTTAAGCATATGGTACAGCAGTGTTAACTCCATGCATGTTGTGAAAC  
AGACCCCCGGAACCTTCTCATCTTGTAATTCTGAAGTTCTATACCCACCGAACAACTCCTCTT  
TTCCCCTTCCCCCTGCCTGCCCCAGCTCTTGGCACCATTATTCTGCTTTCTGTTTTTGAGAGT  
CTGACTACTTAAGATACCTCATACAAGCGGGATCTGGCTTACATTTCTTGAGCATTGTATTCT  
GGAAAAGTGTTTCCTTCTCTGAAAAATGGGTAGAGTTCTGAAGGAGAACTACTGGTCTTATT  
GTACACTTGCTGTACCTATTTTTATTTAACAAATATTCATCTATGGTATAATAAAGATGTCAT  
GGTTGGAAAAAAAAAAAAAAAAAAAAAAAAAAAA

510/615

**FIGURE 506**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96893
><subunit 1 of 1, 173 aa, 1 stop
><MW: 19733, pI: 8.78, NX(S/T): 0
MHWKMLLLLLLLYYNAEASMCHRWSRAVLFPAAHRPKRSSSLPLNPVLQTSLEEVELLYEF
LLAELEISPDLOISIKDEELASLRKASDFRTVCNNVIPKSIPDIRRLSASLSSHPGILKK
EDFERTVLTLAYTAYRTALSHGHQKDIWAQSLVSLFQALRHDLMRSSQPGVPP
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-17

**cAMP- and cGMP-dependent protein kinase phosphorylation sites:**

Amino acids 36-40;84-88;105-109

511/615

**FIGURE 507**

GGCGGCGGGCTGCGCGGAGCGGCGTCCCCTGCAGCCGCGGACCGAGGCAGCGGCGGCACCTGC  
CGGCCGAGCAATGCCAAGTGAGTACACCTATGTGAACTGAGAAGTGATTGCTCGAGGCCTTC  
CCTGCAATGGTACACCCGAGCTCAAAGCAAGATGAGAAAGGCCAGCTTGTTATTTAAAGACAT  
CCTCAAATGTACATTGCTTGTGTTTGGAGTGTGGATCCTTTATATCCTCAAGTTAAATTATAC  
TACTGAAGAATGTGACATGAAAAAATGCATTATGTGGACCCTGACCATGTAAAGAGAGCTCA  
GAAATATGCTCAGCAAGTCTTGCAAGGAATGTCGTCCCAAGTTTGCCAAGACATCAATGGC  
GCTGTTATTTGAGCACAGGTATAGCGTGGACTTACTCCCTTTTGTGCAGAAGGCCCCCAAAGA  
CAGTGAAGCTGAGTCCAAGTACGATCCTCCTTTTGGGTTCGGAAGTTCTCCAGTAAAGTCCA  
GACCCTCTTGGAACCTTGCCAGAGCAGACCTCCCTGAACACTTGAAAGCCAAGACCTGTGCG  
GCGCTGTGTGGTTATTGGAAGCGGAGGAATACTGCACGGATTAGAAGTGGGCCACACCTGAA  
CCAGTTCGATGTTGTGATAAGGTTAAACAGTGCACCAAGTTGAGGGATATTCAGAACATGTTGG  
AAATAAACTACTATAAGGATGACTTATCCAGAGGGCGCACCACTGTCTGACCTTGAATATTAT  
TCCAATGACTTATTTGTTGCTGTTTTTAAAGAGTGTGATTTCAACTGGCTTCAAGCAATG  
GTAAAAAAGGAAACCTGCCATTCTGGGTACGACTCTTCTTTTGGGAAGCAGGTGGCAGAAAAA  
ATCCCACTGCAGCCAAAACATTTTCAAGATTTTGAATCCAGTTATCATCAAAGAGACTGCCTTT  
GACATCCTTCAGTACTCAGAGCCTCAGTCAAGGTTCTGGGGCCGAGATAAGAACGTCCCCACA  
ATCGGTGTCATTGCCGTTGTCTTAGCCACACATCTGTGCGATGAAGTCAGTTGGCGGGTTTT  
GGATATGACCTCAATCAACCCAGAACCTTTGCACACTACTTCGACAGTCAATGCATGGCTGCT  
ATGAACTTTTCAAGCATGCATAATGTGACAACGGAACCAAGTTCCTCTTAAAGCTGGTCAAA  
GAGGGAGTGGTGAAAGATCTCAGTGGAGGCATTGATCGTGAATTTTGAACACAGAAAACCTCA  
GTTGAAAATGCAACTCTAACTCTGAGAGCTGTTTTTGACAGCCTTCTTGATGTATTTCTCCAT  
CCTGCAGATACTTTGAAGTGCAGCTCATGTTTTTAACTTTTAAATTTAAAAACACAAAAAAAT  
TTTAGCTCTTCCCACTTTTTTTTTTCTATTTATTTGAGGTCAAGTGTGTTTTTGCACACCAT  
TTTGTAATGAACTTAAGAATTGAATTGGAAGACTTCTCAAAGAGAATTGTATGTAACGAT  
GTTGTATTGATTTTTTAAGAAAGTAATTTAATTTGTAAACTTCTGCTCGTTTACACTGCACAT  
TGAATACAGGTAACATAATTGGAAGGAGAGGGGAGGTCACTCTTTTGATGGTGGCCCTGAACCT  
CATTCTGGTTCCCTGCTGCGCTGCTTGGTGTGACCCACGGAGGATCCACTCCCAGGATGACGT  
GCTCCGTAGCTCTGCTGCTGATACTGGGTCTGCGATGCAGCGGCGTGAGGCCTGGGCTGGTTG  
GAGAAGGTACAAACCCTTCTCTGTTGGTCTGCCTTCTGCTGAAAGACTCGAGAACCAACCAGG  
GAAGCTGTCCTGGAGGTCCCTGGTTCGGAGAGGGACATAGAATCTGTGACCTCTGACAACCTGTG  
AAGCCACCCTGGGCTACAGAAACCACAGTCTTCCAGCAATTATTACAATTCTTGAATTCCTT  
GGGATTTTTTTACTGCCCTTTCAAAGCACTTAAGTGTAGATCTAACGTGTTCCAGTGTCTGT  
CTGAGGTGACTTAAAAATCAGAACAAAACCTTCTATTATCCAGAGTCATGGGAGAGTACACCC  
TTTCCAGGAATAATGTTTTGGGAACACTGAAATGAAATCTTCCAGTATTATAAATTGTGTA  
TTTAA

512/615

**FIGURE 508**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96897
><subunit 1 of 1, 362 aa, 1 stop
><MW: 41736, pI: 8.80, NX(S/T): 3
MRRPSLLLKDILKCTLLVFGVWILYILKLNYTTEECMDKMMHYVDPDHVKRAQKYAQQVL
QKECRPKFAKTSMAALLFEHRYSDLLPFVQKAPKDSEAESKYDPPFGFRKFSSKVQTLLE
LLPEHDLPEHLKAKTCRRCVVIGSGGILHGLELGHNTLNQFDVVIRLNSAPVEGYSEHVGN
KTTIRMTYPEGAPLSDLEYYSNDLFVAVLFKSVDFNWLQAMVKKETLPFWVRLFFWKQVA
EKIPLQPKHFRILNPVLIKETAFDILQYSEPSRFRWGRDKNVPTIGVIAVVLATHLCDEV
SLAGFGYDLNQPRTPPLHYFDSQCMAAMNFQTMHNVTTETKFLKLKLVKEGVVKDLGGIDR
EF
```

**Important features of the protein:****Transmembrane domains:**

Amino acids 11-27;281-297

**N-glycosylation sites:**

Amino acids 30-34;180-184;334-338

**cAMP- and cGMP-dependent protein kinase phosphorylation sites:**

Amino acids 2-6;109-113;223-227

**N-myristoylation sites:**

Amino acids 146-152;150-156;179-185;191-197

513/615

**FIGURE 509**

GGGCGGACGCAGTGCAGTAAGAGCAGATGGGCGGACCCAAATTTCTTCGGCTTCACGATTTTG  
CCGAGGTCTAGCCCTGCATCCAGCCTTGAAACAGGGTGGGGAGGAGGCAGAAAGGGGAGGGAC  
TGCACTCCCTCTGAGCGTGCTAGCTCCGACTGCCTGACGGATCACCCCTCCGCTCCAACATGG  
CTAGTTCCTCAACGCCGTGACTCAAGCCTGTTGTGCCAGGCAGGGCGCACTCAGCAGCGCAGC  
CCCACAGGTGGCGAAGGCTCCGCGAGAGGGTTCCCGCCAGGCTAGACAGTGGAGTGCCGCACA  
GCGCGCCTTCCAGCCTCGCAGCCGCCACCCTAGCGGTTCCGACCCGGCGCCAGCAGGCCTGCT  
TGGTCGATCTTCGAGCCAAAGATGCGGCGAGGCTGGAAGATGGCTCTGTCTGGGGGGCTGCGG  
TGCTGCCGCCGGGTACTGTCTGGGTGCCAGTGCTCGTTATTGTCCTCGTCGTGCTCTGGTCC  
TACTATGCCTACGTCTTTGAACTCTGCCTGGTTATTTACCTCATACTCTACCATGCCATCTTT  
GTGTTCTTTACCTGGACCTACTGGAAGTCTATCTTTACACTCCACAGCAGCCAAACCAGAAG  
TTCACTTGTCTACACAGACAAGGAGCGCTATGAAAATGAAGAAAGACCTGAGGTCCAGAAG  
CAGATGCTTGTGATATGGCCAAAAGCTACCGGTTACACAAGAACTGGAAGTGGAGGTCAG  
TTCATCCAAAGGCAGCTAGAGAGGCAGCTCAGCAAGTATCTCAGAAAGGCTAAGTCATATATG  
TTCTCAAACTAGCCCTTTTTTTTCCCTCCCATCTTCTGAAAACCACTATGGAGATTTTTCTCCA  
CATTTTATTTCTAAAAAATTTTAAACACATATCAAAGCTGGAAGAATTGTATAGTAAACAAAC  
TGTATACCCCAAACCTGGATTCTTCTGCTAACATTTTTCTGTGTTGCTATATCACATATCTATC  
CACATATGCATACCTCTATTTATCTTTCTGTCAGCCATCTTATGTTTCTGATGCATTTCAAAG  
TAAATAGCTGACATCAGTAAGACATCTACCTAAATATTTTATTCTGTTTTGTAAAATTTACA  
TACAAAACATGCATAATCTTAAGGGTACCATTCCATGTATTTTGAAAAGTGACACATCTGT  
GTAACATAACCCCAATAAAATTGCCATCACCTCAG



514/615

**FIGURE 510**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA98564
><subunit 1 of 1, 143 aa, 1 stop
><MW: 17255, pI: 9.99, NX(S/T): 0
MRRGWKMALSGGLRCCRRVLSWVPVLVIVLVVLWSYYAYVFELCLVIYLLILYHAIFVFFT
WTYWKSIFTLPQQPNQKFHLSYTDKERYENEERPEVQKQMLVDMAKKLPVYTRTGSGGQF
IQRQLERQLSKYLRKAASYMFSN
```

**Important features of the protein:****Transmembrane domain:**

Amino acids 24-45

**N-myristoylation sites:**

Amino acids 11-17;12-18

515/615

**FIGURE 511**

CAGCCGGGGCGATGGCGGGGCTCTGGCTGGGGCTCGTGTGGCAGAAGCTGCTGCTGTGGGGCG  
CGGCGAGTGCCCTTTCCCTGGCCGGCGCCAGTCTGGTCCTGAGCCTGCTGCAGAGGGTGGCGA  
GCTACGCGCGGAAATGGCAGCAGATGCGGCCCCATCCCCACGGTGGCCCGCGCCTACCCACTGGTG  
GGCCACGCGCTGCTGATGAAGCCGGACGGGCGAGGTAAGGGCCGGCGCTCCTCCTGGAGCGCA  
ACGGGGTCCGCGAGCCCCGTTCCACCCCTCCGATCAGCCAGGAACCCGCTGCTTGTGGCGCTGG  
CCGCGAGGAGAGAGGAGCCTGTCAACCCTGTGGAGAATGCACTCCAGTTCTAGTCGTTGCCCT  
TGGCACCCGCCGACACTGCTAGTGGCCCATCCCAAAGTGAGCATTTTCTTTGTGTGTAGCACA  
GGATGCGGTATTTCCAAACCCCTGCCCTCGGTCTTTTCCACCTCACCGCTGCTCAGCTCTCA  
AAGCCCTGCCGTTTCCCTCCTGCCTTGGCTTGGGAAGCCTTAGGAACAGAAGCTCCCTGGGAGC  
ACAGAGCGGTTTTTAAACTGGCCAACACCTTAACGCCAGAGCCGCCCTCCTCTCGCTGCCACT  
TTGGAAAATAAGAGACTAGAGATTCACCTGGACGCTTCCTCCCGGCATCACAAGACTTGACTGC  
TGCTTCAGTTCCCGCTTGACCTTCATACTTTAGCCCTTTAAAGGATGTTACATAATAACAATT  
AAGAGACGGCAGGGCCTTCAGGCAGACTTCTTTGGAGGGTGTCAAACGCCTTGTTTATTAAAG  
AGTGAATTTTTTAAATTAATAATCATGTTTTTAAACAGAGATGGACATTTTATTGATGGAAAAA  
ATCACGTTAAGTTAGAAAGCTCTCAAAGTACCTGGTATTTACAACCTCCCTGTCAGGGAGGGC  
GAACTCGATCTCAGAGTTTTTATTTTATCATCAGGGATTACGTTGAGGTACCCAGAAATGAGAAGA  
TTTGCCCAAAATGGCATATTTTAAATTTGGCCAGACCAGAACCCAGTTTCCCTCTGGGATTAT  
TTGTTAGTAATCGTTTTTACAGGCTGAGCATTAACTCCAAGCTTGAAGGACTTTTTCTC  
ATTTTCACTTGTTTTCTCTAATAAAAAATAATGTCTGTAATTTCAACTTCACAAGATGAGGCCTC  
ATGGAAGAGTGTTTACCAAATATTTAAATACTTTGACAGAAAAAATCAAGCGAACTCTTT  
GCCAACCAATATCATCATGACTGATGTAACAAGTAATCCAACACAGATATGAAAATCACTGG  
TAAAAATCATCTCAGTTAATTCTAAAAGCAGAGCTAACCACCCCTTTTGTCTAAGGCTTTAT  
GGTATTAATAAATAAACTGTACAAAAATATAGATTTTCCCTATCCCTACCCCTGGAAAGTA  
ATATACTGAAGTCTCATCACTGTTTTGGGGATTCCAGTAATTAATACTCTAGTGAACAAA  
GACCTGTTTCAAAACAACCTGTGAGCTGACTGGACTATTTAAAGTAATTCCTTGTTAGTCAC  
TTTCAGAGTGAAGACAATGACGAATACTGTCTTTTACAAAGGGACTTTTTATTCCACCAACAA  
ATTCTGGATTTTGGCATCAGGAAAACCACTGTTCAATTTCCAACACTATATCCAAGTTGTTTG  
AGAAATTATTTAAACTCTTTAACTTAGAGGGTTTTCTTTCTCCTTTACTTGTTAAAGTGACT  
ATATTACAGAGTCACTTTAAGGATTAAATTTATTGCATGCAAAGTTTCTAGATCACTGTCTAG  
AAGTCAGTTAGAGTAAGTTCTTTAGTTGTCAATCAAGCATTTAGTAAGGCCCTGCTTTGTGCC  
CAGTGTTGACCTCAACAAAGTTGGGGATATCAGAATATTCTAAGATACAGTCGTTGTTCCCAA  
GAATCTTGCTTTTACATACAAGAGGTGTTGCGTTTCATTTTGGGGCTAATGTCCAAACGCTG  
GCCTCAGCCATTTACCTTGAAGATTGCAGTTGGCTTCCAACCTGGCCTCTAACTCTAATCTA  
GCATTTTCCAGTCCATTGTGACAAAGTCTGCCTTCCCCAGCTACTCCCAGCTGTTGGACCTGC  
TGCTTTAGAACCACAGATTGGTACCTCGTGCC

516/615

**FIGURE 512**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA107443
><subunit 1 of 1, 178 aa, 1 stop
><MW: 19353, pI: 10.97, NX(S/T): 0
MAGLWLGLVWQKLLLLWGAASALSLAGASLVLSLLQRVASYARKWQQMRPIPTVARAYPLV
GHALLMKPDGRGKGRRSSWSATGSAAPFPPSDQPGTRCLWRWPQERGACHPVENALPVLV
VAPWHPPTLLVPHPKVSIFFVCSTGCGISKPLPSVFSHLTAAQLSKPCRFLLPWLGKP
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-25

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 75-79

**N-myristoylation sites:**

Amino acids 3-9;17-23;145-151

**Amidation site:**

Amino acids 73-77

**Leucine zipper pattern:**

Amino acids 8-30

517/615

**FIGURE 513**

GGCGGCTGGACGAGGACGCTCAGAGCCCAGCTCTCGAGAGTTCAAGCAACCGACGGTTCC  
CCACTGCTCCAGGAGCGGTTACCTGGGCACTCTGTGCCCCCTCCTTCTGTTCGGGCCCCA  
GGCCGAGGACCTGCCAGTAGGGCTCAGTTGCCTGGAGCCCGTTCAGCCCATCCCCCAGTT  
CACTTTGCTTGTGGGATCTCCCCGTTGCTCCTGCCCCTGGACTGAGTGGCAGGCCATCCT  
ACAAGCACCCGGACACTTGACATCAGTGGTGTCAAGACAACCTCTAAGAAGGTTTTCCGTG  
ATCCTGCAAGCCCTGCCTTCCTTCTGCGGATCCTGCCTTCAATTTGATTGCACAGGTACC  
ACAGCAAGCCAGTGCTGTGTGCTCCGAGTTCCAGGGCGTCTCCAGCTCAGCCACTGCAC  
TGAGAACATGGACTCTCTGTGGGGCCCAGGAGCCGGGAGTCACCCCTTTGGGGTCCACAA  
CACCCGGCTGTCCCCAGACTTGTGTCCAGGGAAGATAGTGTTGAGGGCCCTCAAGGAGAG  
CGGGGCAGGGATGCCTGAGCAGGACAAGGACCCTAGAGTCCAAGAGAATCCTGGTGATCA  
GAGAAGGGTCCCCGAGGTCACCGGGGATGCACGGTCTGCATTTTCGGCCCCCTGCGGGACAA  
TGGAGGCCTCTCTCCCTTTGTGCCCCGGGGCCGGGCTCTGCAGACAGACCTCCATGCCCA  
GAGGTGAGAAATCAGATATAACCAGACATCCCAGACCTCCTGGACGAGCTCCTGCACCAA  
CCGAAATGCCATCTCCAGCTCCTACAGCTCCACGGGAGGCTTGCTGGGGCTAAAGCGGAG  
GAGGGGGCCAGCCTCATCCCACTGCCAGCTGACCCCTCAGTTCTCTCAAAGACAGTGAGTGA  
GGACAGGCCTCAGGCTGTCTCTTCAGGTACACCCAGTGTGAAAAGGCAGCAGATATAGC  
ACCAGGGCAGACACTCACCCCTCAGGAATGACTCCTCCACATCCGAGGCCTCTAGGCCCCAG  
TACACACAAGTTTTCCCTGCTGCCACGCGAGGGGAGCCTTTGATGCTGCCACCTCC  
CTTAGAGCTGGGGTACCGGGTCACTGTTGAAGACCTGGACCGGGAGAAGGAGGCGGCCTT  
CCAGCGCATCAACAGTGCACTGCAGGTTGAGGACAAGGCCATCTCGGACTGCAGACCCCTC  
ACGGCCTTCCCACACTTTGTCTCACTTGCAACAGGGGCTTCTGGTCTGCTGCCGTTTC  
TAAAGCACCCAGTATGGATGCACAGCAGGAGACACACAAGTCCCAAGACTGCTGGGCTT  
ACTGGACCCCTTAGCATCTGCTGCAGGGGTCCCCTCTACAGCTCCCATGTCTGGGAAGAA  
GCACAGACCACCAGGCCCCCTGTTCTCCTCCTCAGATCCCCTTCTGCCACCTCTTCTGA  
TTCCCAGGACTCAGCCCAGGTACCTCGCTGATTCTGCCCCCTTCCCAGCTGCAGCAT  
GGATGCGGGCATGAGAAGAACAAGGCATGGCACTTCTGCTCCTGCAGCTGCCGCAGCAGC  
CCCTCCCCGCTCCACATTGAACCCCACTGTTGGGGTCACTACTGGAGTGGATGGAGGCCCT  
TCACATTTCTGGGCCTCAGCCACAGCTGCAGCAGGTGCCAGAGGTCAGAACCAGAGATC  
CCAGACCTCCTGGACCAGCTCGTGCCCCAAATGAATGCCATCTCGAGCCCCTACAGCTC  
TACGGGAGGCCTCCCGGAACAAAAGCGGAAGAGGGGCCAGCCTCATCCCCTGCCAGCTG  
ACCCCTCAGTTCTCAAACACAGTGAGTGAGGACGGACCTCAGGCTGTCTCTTCGGGTCAC  
ACCCAGTGTGAAAAGACGGCAGATACAGCACCAGGGCAGACACTCGCCTCCAGGGGTGGC  
TCCCCCAGATCCCAGGCCTCTAGGCCCCGTATATGCAAGTTTTCCCTGCTGCCACGCAGG  
CGAGGGGAGCCTTTGATGCTGCCACCTCCCTTAGAGATGGGGTACCGGGTCACTGCTGAA  
GACCTGGACCGGGAGAAGGAGGAGGCATTCCAGCGCATCAACAGTGCACTGCAGGTTGAG  
GACCAGGCCATCTAGGACTGCAGACCCTCACGGCCTTCCCACACTTTGTCTCACTTGCA  
ACAGGGGCTTCTGGTCTGCCTGCCGTTTCTAAAGCACCCAGTATGGATGCACAGCAGGAG  
ACACACAAGTCCCAAGACTGCCTGGGCCTAGTGGCCCCCTGCATCTGCTGCACAGGCCT  
GTAGTCCCAGCTACTTGGGAGGCTGAGGCAGGAGAACGGCATAAACCCGGGAGGCAGAGC  
TTGCAGTGAGCTGAGATCGCGCCACTGCACTCCAGCCTGGGTGACAGAGCGAGACTCCGT  
CTC

518/615

**FIGURE 514**

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA107786
><subunit 1 of 1, 428 aa, 1 stop
><MW: 45450, pI: 9.28, NX(S/T): 3
MDSLWGPGAGSHPFVHNTRLSPDLCPGKIVLRALKESGAGMPEQDKDPRVQENPGDQRR
VPEVTGDARSAFRPLRDNGGLSPFVPGPGPLQTDLHAQRSEIRYNQTSQTSWTSSCTNRN
AISSSYSSTGGLLGLKRRRGPASSHCQLTLSSSKTVSEDRPQAVSSGHTQCEKAADIAPG
QTLTLRNDSSSTSEASRPSTHKFPLLPRRRGEPLMLPPPPELGYRVTVEDLDREKEAAFQR
INSALQVEDKAISDCRPSRPSHTLSSLATGASGLPAVSKAPSMDAQQETHKSQDCLGLLD
PLASAAGVPSTAPMSGKKHRPPGPLFSSSDPLPATSSDSQDSAQVTS LI PAF FPAASMDA
GMRRTRHGTSAPAAAAAAPRSTLNP TLGSLLEWMEALHISGPQPQLQQVPRGQNQRSQT
SWTSSCPK
```

**Important features of the protein:****N-glycosylation sites:**

Amino acids 105-109;187-191

**Glycosaminoglycan attachment site:**

Amino acids 38-42

**N-myristoylation sites:**

Amino acids 15-21;130-136;180-186;307-313;361-367

**Amidation site:**

Amino acids 315-319

**Prokaryotic membrane lipoprotein lipid attachment site:**

Amino acids 106-117

519/615

**FIGURE 515**

GTCAGGGCCAGGGTGAGCGCCCGACTCCGAGCTGTCCCCGCTCCCGGCGCGGCGCTCCGCTCT  
CAGCCACCTCACGGCTGCCAGGAGTGCGCGGGAGTTTGCCCCGGAGCGCGGGGAAGTTTCCTC  
CGAAGCTGCGCTCCTGGAACAGCAGCACCTGCAAGCGCCCGCAGCGGCCCGCGAGGTTACTT  
TATGGAATTGGGCTCTTAGAGAACAAGAAAAGACTGAAGTTTTACGGGAAAACAAATCATGTG  
GTCTTCAGATTCTGAAATAAGGAGAAATGAGCCATCTGAAATGGTCATGAACCCCAAACAAG  
TCTTCCTCTCTGTGCTGATATTTGGAGTAGCTGGGCTACTCCTCTTCATGTATTTGCAAGTCTGG  
ATTGAAGAACAACATACAGGGAGAGTGGAGAAGAGAAGAGAACAAAAGTAAGTTTCAGGATGG  
GGACCAGTGAAGTACTTGCGGCCTGTACCCAGAATCATGAGTACAGAAAAAATCCAGGAACAT  
ATCACCACCAGAACCCCAAGTTTCACATGCCTGAGGATGTACGAGAAAAAAGGAAAATCTT  
CTACTCAATTCTGAGAGATCTACTAGGCTCTTAACAAAGACCAGTCATTCACAAGGAGGGGAT  
CAAGCTTTAAGTAAGTCCACAGGGTCACCAACAGAGAAGTTGATTGAAAAACGTCAAGGAGCT  
AAGACTGTTTTTAACAAGTTCAGCAACATGAATTGGCCAGTGGACATTACCCCTTTAAACAAA  
AGTTTAGTCAAAGATAATAAATGGAAGAAAAGTGAAGAGACCCAAGAGAAACGAAGGTCTTTC  
CTTCAGGAGTTTTGCAAGAAATACGGTGGGGTGAGTCATCATCAGTCACATCTTTTTCATACA  
GTATCCAGAATCTATGTAGAAGATAAACAAAAATCTTATATTGTGAGGTACCTAAGGCTGGC  
TGTTCCAATTGGAAAAGAATTCTGATGGTACTAAATGGATTGGCTTCCTCTGCATACAACATC  
TCCCACAATGCTGTCCACTACGGGAAGCATTGAAGAAGCTAGATAGCTTTGACCTAAAAGGG  
ATATATACCCGCTTAAATACTTACACCAAGCTGTGTTTGTTCGTGATCCCATGGAAAGATTA  
GTATCAGCCTTTAGGGACAAATTTGAACACCCCAATAGTTATTACCATCCAGTATTCGGAAAG  
GCAATTATCAAGAAATATCGACCAAAATGCCTGTGAAGAAGCATTAAATTAATGGATCTGGAGTC  
AAGTTCAAAGAGTTTATCCACTACTTGCTGGATTCCCACCGTCCAGTAGGAATGGACATTCAC  
TGGGAAAAGGTCAGCAAACTCTGCTATCCGTGTTTGATCAACTATGATTTTGTAGGGAAATTT  
GAGACTTTGGAAGAAGATGCCAATTACTTTTTTACAGATGATCGGTGCTCCAAAGGAGCTGAAA  
TTTCCCAACTTTAAGGATAGGCACTCTTCCGATGAAAGAACCAATGCTCAAGTCGTGAGACAG  
TATTTAAAGGATCTGACTAGAACTGAGAGACAATTAATCTATGACTTTTTATTACTTGGACTAT  
TTAATGTTTAATTATACAACCTCCACTTTTGAGTTTGCATTCAATTTCTAAAACCCTGTATAT  
ACTTAATGATGATAAGTTCAAATCAGCTGTAATTTTTCTATAATTCTCTGTATGACAGAAATT  
TAACCAAGTGCAGTTGTCTTGATTTAATGTAGATTTTTTACCAAATAGTATGACACCAATTGGC  
ACAAAGTTATAGGAAAATCACCTACAGGAGATGTAAACAACCTTGAGTTGCTCTAAAATGTTTG  
GAAAAGAGCTGCTTTTGCATTATGAATTATATTGTTGAAGCAATAACCTAGCCAGCTGTTGCA  
TTAGCTAAAGCAGCCTCTTGCAATGGTAGGAAAAAAGGATCTCAAATAGCATGAGTGTATGTC  
TATATCCTGAAATTTATTGTCTAAAATGCATGAATATATTTTTAGCAGTCTGTGGCATATTA  
TCAAACCTGTTGAATTGTTTTCTTACACCCTGGAAATCTTTCTATCAACTATAATGATAAATCC  
ATTTTGAAGTGATATTTTGGACTTAGGCATTTTACTTTAGATTGGAAGGCATTATGTGATTTACA  
ATATGAGAATATAGCAGAAAAACCA

520/615

**FIGURE 516**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108682
><subunit 1 of 1, 443 aa, 1 stop
><MW: 52021, pI: 9.63, NX(S/T): 4
MQPSEMVMNPKQVFLSVLIFGVAGLLLFMYLQVWIEEQHTGRVEKRREQKVTSGWGPVKY
LRPVPRIMSTEKIQEHITNQNPKEHMPEDVREKKENLLLNSERSTRLLTKTSHSQGGDQA
LSKSTGSPTEKLEKRGAKTVFNKFSNMNWPVDIHPLNKSLVKDNKWKKTETQEKRRS
FLQEFCKKYGGVSHHQSHLFHTVSRIYVEDKHKILYCEVPKAGCSNWKRILMVLNGLASS
AYNISHNAVHYGKHLKKLDSFDLKGITYTRLNTYTKAVFVRDPMERLVSAFRDKFEHPNSY
YHPVFGKAIKKYRPNACEEALINGSGVKFKEFIHYLLDSHRPVGMDIHWEKVSCLCYP
LINYDFVGKFETLEEDANYFLQMGAPKELKFPNFKDRHSSDERTNAQVVRQYLKDLTRT
ERQLIYDFYYLDYLMFNYYTPLL
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-24

**N-glycosylation sites:**

Amino acids 159-163;243-247;324-328;437-441

**Glycosaminoglycan attachment site:**

Amino acids 53-57

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 177-181

**Tyrosine kinase phosphorylation site:**

Amino acids 329-337

**N-myristoylation sites:**

Amino acids 116-122;236-242

521/615

**FIGURE 517**

GGAACTTCCCAGGCACCCTGTGTGGCCGCACTGCTCCCTCTGGCCCAACCATGCCTCTGTCCAGCCACCTGCTGC  
CCGCCTTGGTCTCTTCCCTGGCAGGGTCTCAGGCTGGGCCTGGGTCCCCAACCCTGCAGGAGCCCTGGCCAGG  
CCGTGTGCAACTTTCGTGTGACTGCAGGGACTGCTCAGATGAGGCCAGTGTGGTTACCACGGGGCCTCGCCCA  
CCCTGGGCGCCCCCTTCGCCTGTGACTTCGAGCAGGACCCCTGCGGCTGGCGGGACATTAGTACCTCAGGCTACA  
GCTGGCTCCGAGACAGGGCAGGGGCCGCACTGGAGGGTCTGGGCCTCACTCAGACCACACACTGGGCACCGACT  
TGGGCTGGTACATGGCCGTTTGAACCCACCGAGGGAAAGAGGCATCCACCGCAGCCCTGCGCTCGCCAACCCTGC  
GAGAGGCAGCCTCCTCTTGAAGCTGAGGCTCTGGTACCACGCGGCCTCTGGAGATGTGGCTGAACCTGCGGGTGG  
AGCTGACCCATGGCGCAGAGACCCTGACCCTGTGGCAGAGCACAGGGCCCTGGGGCCCTGGCTGGCAGGAGTTGG  
CAGTGACCACAGGGCCGATCCGGGGTGAATTCGAGTGACCTTCTTGCCACCCGAAATGCCACCCACAGGGGCG  
CTGTGGCTCTAGATGACCTAGAGTTCTGGGACTGTGGTCTGCCCACCCCCAGGCCAAGTGTCCCCGGGACACC  
ACCACTGCCGAACAAGGTCTGCGTGGAGCCCCAGCAGCTGTGCGACGGGGAAGACAAGTGTGGGGGACCTGTCTG  
ATGAGAACCCTCACTCAGCTGTGGCCGCCACATAGCCACCGACTTTGAGACAGGCCTGGGCCCATGGAACCGCTCGG  
AAGGCTGGTCCCGGAACCACCGTGTGGTGGTCTGAGCGCCCTCCTGGCCACGCGCTGACCAAGCCGGAACA  
GTGCACAGGGTCTCTTCCCTGGTCTCCGTGGCCGAGCCTGGCACCCTGCTATACTCTCCAGCCCCGAATTCCAAG  
CCTCAGGCACCTCCAAGTGTCTGCTGGTCTTCTATCAGTACCTGAGTGGGTCTGAGGTGGCTGCTCCAGCTGT  
TCCTGCAGACTCTGGGGCCCGGCGCCCCCGGGCCCCCGTCTGCTGCGGAGGCGCCGAGGGGAGCTGGGGACCG  
CCTGGGTCCGAGACCGTGTGACATCCAGAGCGCCTACCCCTCCAGATCCTCCTGGCCGGGCGAGACAGGCCCGG  
GGGGCGTCTGGGTCTGGACGACCTCATCTGTCTGACCACTGCAGAGTCTCGAGGTGTCCACCCTGCAGC  
CGCTGCCTCCTGGGCCCCGGGCCCCAGCCCCCAGCCCTGCCGCCAGCTCGCGGCTCCAGGATTCCTGCAAGC  
AGGGGCATCTTGCTGCGGGGACCTGTGTGTGCCCGGAACAAGTGTGTGACTTCGAGGAGCAGTGCAGAGGGG  
GCGAGGACGAGCAGGCCTGTGGCACCACAGACTTTGAGTCCCCGAGGCTGGGGGCTGGGAGGACGCCAGCGTGG  
GGCGGTGCAGTGGCGGCGTGTCTCAGCCCAGGAGAGCCAGGGGTCCAGTGCAGCTGCTGCTGGGCACTTCTGT  
CTCTGCGAGCGGGCCTGGGGGCGAGCTAGGCGCTGAGGCCCGGGTCTCACACCCCTCTGGCCCTTCTGGCCCCA  
GCTGTGAACCTCACTGGCTTATTATTTACAGAGCCAGCCCCGAGAGGTCTCCTGTAACCTTTGAGCGGGACACAT  
GCAGCTGGTACCCAGGCCACCTCTCAGACACACTGGCGTGGGTGGAGAGCCGCGGCCCTGACCACGACCACA  
CCACAGGCCAAGGCCACTTTGTGCTCCTGGACCCACAGACCCCTGGCCTGGGGCCACAGTGGCCACCTGCTCT  
CCAGGCCCAGGTGCCAGCAGCACCACGGAGTGTCTCAGCTTCTGGTACCACCTCCATGGGCCCCAGATTGGGA  
CTCTGCGCCTAGCCATGAGACGGGAAGGGGAGGAGACACACCTGTGGTGGCGGTGAGGCACCCAGGGCAACCGCT  
GGCAGGAGGCTGGGCCACCCCTTTCCACCAGCCTGGCTCCCATGCCAGTACCAGCTGCTGTTCCGAGGGCCCTCC  
GGGACGGATACACGGCACCATGGCGCTGGACGATGTGGCGTGGCGCGGGGCCCTGCTGGGCCCCTAATTACT  
GCTCCTTTGAGGACTCAGACTGCGGCTTCTCCCCTGGAGGCCAAGGTCTCTGGAGGCGGCAGGCCAATGCCTCGG  
GCCATGCTGCTGGGGCCCCCAACAGACCATAACCACTGAGACAGCCCAAGGGCACTACATGGTGGTGGACACAA  
GCCCAGACGCACTACCCCGGGGCCAGACGGCCTCCCTGACCTCCAAGGAGCACAGGCCCTGGGCCAGCCTGCTT  
GTCTGACCTTCTGGTACCACGGGAGCCTCCGCGAGCCAGGCACCTGCGGGTCTACCTGGAGGAGCGCGGGAGGC  
ACCAGGTGCTCAGCCTCAGTGGCCACGGCGGGCTTGCTGGCGCCTGGGCAGCATGGACGTGCAGGCGGAGGAG  
CCTGGAGGGTGGTGTGTTGAGGCAGTGGCGCGAGGCGTGGCACACTCCTACGTGGCTCTGGATGATCTGCTCCTCC  
AGGACGGGCCCTGCCCTCAGCCAGGTTCTGTGATTTTGAAGTCTGGCCTGTGTGGCTGGAGCCACCTGGCCGGGC  
CCGGCCTGGGCGGATACAGCTGGGACTGGGGCGGGGAGCCACCCCTCTCGTTACCCCCAGCCCCCTGTGGACC  
ACACCTGGGCGACAGAGGCAGGCCACTTTGCCCTTCTTTGAAACTGGCGTGGTGGGCCCCGGGGCGGGCGCCT  
GGCTGCGCAGCGAGCCTCTGCCGGCCACCCAGCCTCCTGCCTCCGCTTCTGGTACCATGGGTTTTCTGTAGC  
ACTTCTACAAGGGGGAGCTGAAGTACTGCTGCACAGTGTCTCAGGGCCAGCTGGCTGTGTGGGGCGCAGGCGGGC  
ATCGGCGGCACCAAGTGGCTGGAGGCCAGGTGGAGGTAGCCAGTGCCAAGGAGTTCCAGATCGTGTGTTGAAGCCA  
CTCTGGGCGGCCAGCCAGCCCTGGGGCCATTGCCCTGGATGACGTGGAGTATCTGGCTGGGCAGCATTGCCAGC  
AGCCTGCCCCCAGCCCGGGGAACACAGCCGACCCGGGTCTGTGCCAGCTGTGGTTGGCAGTGCCCTCCTATTGC  
TCATGCTCCTGGTGTCTGGGACTTGGGGGACGCGCTGGCTGCAGAAGAGGGGAGCTGCCCTTCCAGAGCA  
ACACAGAGGCCACAGCCCTGGCTTTGACAACATCCTTTTCAATGCGGATGGTGTACCCCTCCCGGCATCTGTCA  
CCAGTGATCCGTAGACCACCCAGACAAGGCCCGCTTCTCAGTGACATCCAGCACTTGGTCAGACCCTAGCC  
AGGGACCGGACACCTGCCCCGCCCAGGCTGGGACAGGTGCAGGTCTCAGGATATGCTGAGGCCTGGGCGTCCCC  
TGCCCTGTGCTGACTCTGTGCTCTGTGAATAAACACCTGGCCCATGAGGGCGCCCCCAAAAAAAAAAAAAA  
AAAAAAAAAAAAA



522/615

**FIGURE 518**

```
>>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108684
>>subunit 1 of 1, 1137 aa, 1 stop
><MW: 122776, pI: 6.00, NX(S/T): 4
MPLSSHLLPALVLFFLAGSSGWAVPNHCRSPGQAVCNFVCDRCDSDEAQCQYHGASPTL
GAPFACDFEQDPCGWRDISTSGYSWLRDRAGAALEGPGPHSDHTLGTDLGWYMAVGTHRG
KEASTAALRSPPTLREAASSCKLRLWYHAASGDVAELRVELTHGAETTLTWQSTGPWGPW
QELAVTTGRIRGDFRVTF SATRNATHRGAVALDDLEFWDCGLPTPQANCPPGHHHCQNKV
CVEPQQLCDGEDNCGDLSDENPLTCGRHIATDFETGLGPWNRSEGSNRHRAGGPERPSW
PRRDHSRNSAQGSFLVSVAEPTGPAILSSPEFQASGTSNCSLVFYQYLSGSEAGCLQLFL
QTLGPGAPRAPVLLRRRRGELGTAWVRDRVDIQSAYPFQILLAGQTGPGGVVGLDDLILS
DHCRPVSEVSTLQPLPPGPAPAPQPLPPSSRLQDSCKQGHLAGDLCVPPEQLCDFEEQ
CAGGEDEQACGTTDFESPEAGGWEDASVGRQLQWRRVSAQESQGSSAAAAGHFLSLQRAWG
QLGAEARVLTPLLGPSPGSCLEHLAYYLQSQPREVSCNFERDTC SWYPGHLSDTHWRWVE
SRGPDHDHTTGQGHFVLLDPTDPLAWGHSALLSRPQVPAAPTECLSFYHLHGPDIGTL
RLAMRREGEETHLWSRSGTQGNRWHEAWATLSHQPGSHAQYQLLFEGLRDGYHGTALDD
VAVRPGPCWAPNYCSFEDSDCGFSPGGQGLWRRQANASGHAAWGPPTDHTTETAQGHYMV
VDTSPDALPRGQTASLT SKEHRPLAQPACLT FWYHGSLRSPGTLRVYLEERGRHQVLSLS
AHGGLAWRLGSMVDVQAERAWRVVFEAVAAGVAHSYVALDLLLLQDGPQPGSCDFESGL
CGWSHLAGPGLGGYSWDWGGGATPSRYPPQPPVDHTLGTEAGHFAFFETGVLGPGGRAAWL
RSEPLPATPASCLRFWYHMGFPEHFYKELKVLHSAQQQLAVWGAGGHRRHQWLEAQVE
VASAKEFQIVFEATLGGQPALGPALDDVEYLAGQHCQQPAPSPGNTAAPGSVPAVVGSA
LLLLMLLVLLGLGGRWLQKKGSCPFQSNTEATAPGFDNILFNADGVTLFASVTSDF
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-20

**Transmembrane domain:**

Amino acids 1075-1092

**N-glycosylation sites:**

Amino acids 203-207;281-285;339-343;756-760

**cAMP- and cGMP-dependent protein kinase phosphorylation sites:**

Amino acids 514-518;1100-1104

**N-myristoylation sites:**

Amino acids 32-38;55-61;61-67;106-112;116-122;336-342;350-356;409-415;  
523-529;540-546;678-684;707-713;791-797;870-876;921-927;  
937-943;954-960;1036-1042;1071-1077

**Amidation site:**

Amino acids 1093-1097

**Cell attachment sequence:**

Amino acids 191-194

523/615

**FIGURE 519**

GCAGGGGAGCTCCGAGTGTCCACAGGAAGGGAACTATCAGCTCCTGGCATCTGTAAGG**ATGCT**  
GTCCATGCTGAGGACAATGACCAGACTCTGCTTCCTGTTATTCTTCTCTGTGGCCACCAGTGG  
GTGCAGTGCAGCAGCAGCCTCTTCTCTTGAGATGCTCTCGAGGGGAATTCGAAACCTGTGCCTT  
CTCCTTTTCTTCCCTGCCTAGAAGCTGCAAAGAAATCAAGGAACGCTGCCATAGTGCAGGTGA  
TGGCCTGTATTTTCTCCGCACCAAGAATGGTGTGTCTACCAGACCTTCTGTGACATGACTTC  
TGGGGGTGGCGGCTGGACCCTGGTGGCCAGCGTGCACGAGAATGACATGCGTGGGAAGTGCAC  
GGTGGGTGATCGCTGGTCCAGTCAGCAGGGCAACAAAGCAGACTACCCAGAGGGGGATGGCAA  
CTGGGCCAACTACAACACCTTTGGATCTGCAGAGGCGGCCACGAGCGATGACTACAAGAACCC  
TGGCTACTACGACATCCAGGCCAAGGACCTGGGCATCTGGCATGTGCCCAACAAGTCCCCCAT  
GCAGCATTGGAGAAACAGCGCCCTGCTGAGGTACCGCACCAACACTGGCTTCCTCCAGAGACT  
GGGACATAATCTGTTTGGCATCTACCAGAAATACCCAGTGAAATACAGATCAGGGAAATGTTG  
GAATGACAATGGCCCAGCCATACCTGTGGTCTATGACTTTGGTGATGCTAAGAAGACTGCATC  
TTATTACTCACCGTATGGTCAACGGGAATTTGTTGCAGGATTCGTTCAGTTCCGGGTGTTTAA  
TAACGAGAGAGCAGCCAACGCCCTTTGTGCTGGGATAAAAGTTACTGGCTGTAACACTGAGCA  
TCACTGCATCGGTGGAGGAGGGTTCTTCCACAGGGCAAACCCCGTCAGTGTGGGGACTTCTC  
CGCCTTTGACTGGGATGGATATGGAACACGTTAAGAGCAGCTGCAGTCGGGAGATAACGGA  
GGCGGCTGTACTCTTGTCTATAGAT**TGAG**ACAGAGCTCTGCGGTGTCAGGGCGAGAACCCATC  
TTCCAACCCCGGCTATTTGGAGACGGAAAACTGGAATTCTAACAAGGAGGAGAGGAGACTAA  
ATCACATCAATTTGCA

524/615

**FIGURE 520**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108701
><subunit 1 of 1, 325 aa, 1 stop
><MW: 36212, pI: 8.68, NX(S/T): 1
MLSMRLRTMTRLCFLLFFSVATSGCSAAAASSLEMLSREFETCAFSFSSLPRSCKEIKERC
HSAGDGLYFLRTKNGVVYQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDRWSSQOGNKA
DYPEGDGNWANYNTFGSAEAATSDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSALLR
YRTNTGFLQRLGHNLFGIYQKYPVKYRSGKCWNDNGPAIPVVYDFGDAKKTASYYSYGQ
REFVAGFVQFRVFNNERAANALCAGIKVTGCNTEHHCIGGGGFFPQGKPRQCGDFSADFWD
DGYGTHVKSSCSREITEAAVLLFYR
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-26

**Glycosaminoglycan attachment site:**

Amino acids 86-90

**N-myristoylation sites:**

Amino acids 23-29;88-94;127-133;136-142;265-271

525/615

**FIGURE 521**

GATCAGTGTGTGAGGGAAGTCCATCATGAGGTCTGACAAGTCAGCTTTGGTATTTCTGCTCCTGCAGCTCTTCT  
GTGTTGGCTGTGGATTCTGTGGGAAAGTCCTGGTGTGGCCCTGTGACATGAGCCATTGGCTTAATGTCAAGGTCA  
TTCTAGAAGAGCTCATAGTGAGAGGCCATGAGGTAACAGTATTGACTCACTCAAAGCCTTCGTTAATTGACTACA  
GGAAGCCTTCTGCATTGAAATTTGAGGTGGTCCATATGCCACAGGACAGAAACAGAAAGAAATGAAATATTTGTTG  
ACCTAGCTCTGAATGTCTTGCCAGGCTTATCAACCTGGCAATCAGTTATAAAATTAATGATTTTTTTGTTGAAA  
TAAGAGGAAGTTTAAAAATGATGTGTGAGAGCTTTATCTACAATCAGACGCTTATGAAGAAGCTACAGGAAACCA  
ACTACGATGTAATGCTTATAGACCCTGTGATTCCCTGTGGAGACCTGATGGCTGAGTTGCTTGCAGTCCCTTTTG  
TGCTCACACTTAGAATTTCTGTAGGAGGCAATATGGAGCGAAGCTGTGGGAAACTTCAGCTCCACTTTCTCTATG  
TACCTGTGCCTATGACAGGACTAACAGACAGAATGACCTTTCTGGAAAGAGTAAAAAATTCATGCTTTTCAGTTT  
TGTTCCACTTCTGGATTGAGGATTACGACTATCATTTTTGGGAAGAGTTTTATAGTAAGGCATTAGGAAGGCCCA  
CTACATTATGTGAGACTGTGGGAAAAGCTGAGATATGGCTAATACGAACATATTGGGATTTTGAATTTCTCAAC  
CATACCAACCTAACTTTGAGTTTGTGGAGGATTGCACTGTAAACCTGCCAAAGCTTTGCCTAAGGAAATGGAAA  
ATTTTGTCCAGAGTTCAGGGGAAGATGGTATTGTGGTGTCTCTCTGGGGTCACTGTTTCAAAATGTTACAGAAG  
AAAAGGCTAATATCATTGCTTCAGCCCTTGCCAGATCCCACAGAAGGTGTTATGGAGGTACAAAGGAAAAAAC  
CATCCACATTAGGAGCCAATACTCGGCTGTATGATTGGATACCCAGAAATGATCTTCTTGGTTCATCCCAAAACCA  
AAGCTTTTATCACTCATGGTGAATGAATGGGATCTATGAAGCTATTTACCATGGGGTCCCTATGGTGGGAGTTC  
CCATATTTGGTGATCAGCTTGATAACATAGCTCACATGAAGGCCAAAGGAGCAGCTGTAGAAATAAACTTCAAAA  
CTATGACAAGCGAAGATTTACTGAGGGCTTTGAGAACAGTCATTACCGATTCTCTTATAAAGAGAATGCTATGA  
GATTATCAAGAATTCACCATGATCAACCTGTAAAGCCCTAGATCGAGCAGTCTTCTGGATCGAGTTTGTCTATGC  
GCCACAAAGGAGCCAAGCACCTGCGATCAGCTGCCCATGACCTCACCTGGTTCCAGCACTACTCTATAGATGTGA  
TTGGGTTCTGCTGACCTGTGTGGCAACTGCTATATTCTTGTTCACAAAATGTTTTTTATTTTCTGTCAAAAAT  
TTAATAAAACTAGAAAGATAGAAAAGAGGGAATAGATCTTTCCAAATTCAGAAAGACCTGATGGGGTAATCCTG  
TTAATTCAGCCACATAGAATTTGGTGAAGAACCTTGCTATTTTCATATTATCTATTCTGTTATTTTATCTTAGCT  
ATATAGCCTAGAATTCATGATCATGAGGTTGTGAGTATATCTCATTCTTTCTGTTGATTTTCTTAGGTGTCTTT  
ACTCTCTTCTCTCACTTTGTGACACAAGGACATGAATACATCTAAATTTTCTATTTCTGATATGACTGTTTTGA  
TGATGTCTATTACTTCTATAACCTTAAGTGATAGGGTGACATGCAATATGATTATTCCTGGTGTGCGCCCAACAC  
ATGGATATAAAGAGGTAAAAAACTTAAATTCACAAAATTCAGTAAACCACACAAATCAGGTAAGTGTTCTATGA  
GATTAGCTGGCTATGAGAAACATAATGATGTTTCTTTTCAATTTAAATAAGCCTTTCTACATAGCCAGCATCAG  
TGATCTCAGAAAATAAATTGCTAATAATGATGACATGGCATTATGCTTAGAAAAGTTTGCTGTATTTCCATAGAC  
CTCATCTAGATGTGATGGCCTACATTTCTGCCATCACTCAACCAATACTTTTTCTGTTTTCTTGATGATAAAAA  
GACCTTTCTCATGATTGCCATCAAATAACAAAAGAACTATTTTTTTCTCACATAGAGAACATGTCAGTAAGAT  
ATTCAGGTGAACAGATATTTTTGGGATTAGTAACTATTTGAAATATGTGGTGATAATTACTGAGTTTATAAAAT  
TTATTTGATAGTACACTTAAAGAAGATTATATGTTTATCTTTAAAAATGATGAATACTCATAATTCTTATCTC  
TATAATCAAAGTATAATTTACTGTAGAAAATAAAGAGATGCTTGTTCTGAAAGTAAGATCAGTGAAGTGCCTT  
TCAGTCTCAATCTTTGAGAATTGTAAATTCATCAAATAATTGCTTACATAGTAAAAATTTAAGGTATTAGAAAAC  
CTGCATAACAAATAGTATTATATATTAATATTTTGATATGTAAAGCTCTACACAAAGCTAAATATAGTGAATA  
ATGTTTACACTAGTAAGCAAATATGTTAATCTTCTCATTTTTTTACTGTGATATAATCTTAGTGATATGCCTATT  
AATAGTTTTAAATAAATAAATTGGCTTATCTGGCTTTTTGAAAATTTGAAATTTTACAGATGTTGATTAGGTA  
TATCTACAAATTAATTTCAATTTTAAATGATGATATAAAATAAATATAAGTATTTTTCTGTGTATGTATACA  
ATAAATATAAATAAATTTGTTTACTGTTTTGAAAGTTTCTTAAGTTTTA

526/615

**FIGURE 522**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108720
><subunit 1 of 1, 527 aa, 1 stop
><MW: 60284, pI: 8.31, NX(S/T): 3
MRSDKSALVFLLLQLFCVCGFCGKVLVWPCDMSHWLNVKVILEELIVRGHEVTVLTHSK
PSLIDYRKPSALKFEVVHMPQDRTEENEIFVDLALNVLPGLSTWQSVIKLNDFVEIRGT
LKMMCESFIYNQTLMKKLQETNYDVMLIDPVI PCGDLMAELLAVPFVLTLRISVGGNMER
SCGKLPAPLSYVPVPM TGLTDRMTFLERVKNSMLSVLFHFWIQDYDYHFWEFYSKALGR
PTTLCETVGKAEIWLIRTYWDFEFPQPYQPNFEFVGGLHCKPAKALPKEMENFVQSSGED
GIVVFSLSLSLFQNVTEEKANIIASALAQIPQKVLWRYKGKKPSTLGANTRYDWIPQNDL
LGHPKTKAFITHGGMNGIYEAIYHGVPVMGVPIFGDQLDNIAHMKAKGAAVEINFKTMTS
EDLLRALRTVITDSSYKENAMRLSRIHHDQPVKPLDRAVFWIEFVMRHKGAKHLRSAHD
LTWFQHSIDVIGFLLTCVATAIFLFTKCFLFSCQKFNKTRKIEKRE
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-21

**Transmembrane domain:**

Amino acids 489-510

**N-glycosylation sites:**

Amino acids 131-135;313-317;518-522

**cAMP- and cGMP-dependent protein kinase phosphorylation sites:**

Amino acids 67-71;340-344

**Tyrosine kinase phosphorylation sites:**

Amino acids 122-131;136-144

**N-myristoylation sites:**

Amino acids 19-25;276-282;373-379;377-383

**Amidation site:**

Amino acids 338-342

527/615

**FIGURE 523**

GGCTGCGGGGTCGGCACGGAAGATGCACGCGAGGCTCCTGGGGCTCTCGGCCCTGCTGCAGGC  
GGCCGAACAGAGCGCGCGCCTTTACACCGTGGCTTACTACTTCACCACAGGACGGCTTCTGTG  
GGGGTGGCTGGCCCTTGCTGTCCTCCTGCCCGGGTTCTTGGTCCAGGCCCTGAGCTACCTGTG  
GTTCCGAGCAGACGGGCATCCAGGGCATTGCTCCTTGGTGATGCTGCACCTCCTACAGCTTGG  
TGTTTGGAAGCGGCACTGGGACGCTGCACTGACCAGTCTGCAGAAGGAAGTGGAGGCTCCCCA  
CCGAGGCTGGCTGCAGCTGCAGGAGGCCGACCTGTGCGGCCCTTCGACTCTTGGAGGCCCTGCT  
GCAGACTGGGCCCCACCTGCTGCTTCAGACATATGTTTTCTAGCCTCAGACTTCACAGATATT  
GTGCCAGGGGTGAGCACCTGTTCCTGGTCTCACTCTCCTGGGCACTGGTGTCTTACACT  
CGCTTCATGGGCTTCATGAAGCCAGGCCACCTGGCCATGCCATGGGCCGCCCTCTTCTGCCAG  
CAGCTCTGGAGGATGGGCATGTTGGGAACCCGCGTCTGAGTCTGGTCTGTTCTACAAAGCC  
TACCACTTTTGGGTTTTTGTGGTTGCAGGTGCCCACTGGCTGGTGATGACATTCTGGCTTGTG  
GCCAGCAGAGTGACATCATCGACAGCACCTGCCACTGGAGGCTGTTCAACCTGCTCGTGGGG  
GCCGTGTACATCCTCTGCTACCTCAGCTTCTGGGACAGCCCTTCTAGAAATAGGATGGTCACG  
TTCTACATGGTCATGCTGTTGGAGAACATCATCTGTTGCTGTTGGCCACCGACTTCTCCAG  
GGGGCATCGTGGACCAGCCTGCAGACCATAGCTGGGGTCTGTCTGGATTTCTGATTGGCAGT  
GTCTCACTGGTAATTTATTACAGCCTGCTGCATCCAAAATCCACAGACATCTGGCAGGGCTGC  
CTAAGGAAGTCTGTGGCATTGCAGGAGGTGATAAAACAGAGAGAAGAGATTCTCCCCGGGCC  
ACAGATCTAGCTGGGAAGAGAACCGAGAGCTCAGGCTCATGCCAAGGGGAAGTTATGAACCA  
ACCATTTTAGGGAAGCCCCCTACCCCTGAGCAGGTCCCCCAGAGGCTGGGCTGGGGACCCAG  
GTTGCTGTGGAGGACTCTTTCCTCAGTCATCACCCTGGCTGTGGGTGAACTTGCCCTAAAA  
ACAGGAAATGTGTCTAAGATCAATGCCGCCTTTGGAGATAACAGTCTGCCTATTGTCCACCT  
GCATGGGGGTTGAGTCAACAGGACTACCTGCAGAGAAAGGCCTTGTCTGCCAGCAAGAGCTC  
CCATCCTCATCCCGTGACCCCTCAACCTTAGAGAACAGCTCTGCGTTTGAAGGTGTCCCTAAA  
GCAGAGGCCGACCCATTGGAAACCTCAAGTTACGTATCTTTTGCCAGCGATCAGCAGGATGAA  
GCACCTACCCAGAACCCAGCAGCCACGCAGGGGGAGGGCACCCCAAAGGAAGGAGCTGACGCT  
GTTTCTGGGACACAGGGGAAGGGGACAGGTGGGCAGCAGAGAGGAGGGGAAGGACAGCAGAGT  
TCCACGTTGTACTTCAGCGCCACTGCAGAAGTGGCCACATCCTCACAACAAGAAGGCAGCCCA  
GCTACTCTGCAAACGGCCCACTCTGGAAGGAGGCTGGGAAAGAGCAGCCCTGCCAGCCTGCA  
TCGCCCCACCCAGTGGGCTTGGCGCCCTTCCCCGACACCATGGCCGACATTAGCCCCATCCTA  
GGCACAGGCCCATGTAGAGGCTTCTGCCCCAGTGCAGGCTTCCCTGGAAGAACCCTCAGTATC  
TCAGAGCTAGAGGAGCCGCTGGAGCCCCAAAAGGGAGCTAAGTCACCATGCAGCTGTTGGTGTG  
TGGGTGTCATTGCCACAGCTGAGGACTGCCCATGAGCCCTGCCTCACGTCCACCCCTAAGTCT  
GAGTCTATCCAAACGGACTGCAGCTGCAGGGAACAGATGAAGCAAGAGCCGAGTTTTTTCATC  
**TGAC**CCACAGTCATGGTGGGATAAGACAACAGGCTGACAAACCAAGCTGGCCATTTGGTACCGT  
GAGAAAGGAAATCCCCTTCTGACACCTGTGTCCTTGGGCACATCACTGTCACCTCTGAATCT  
CCATCTGCATCCCTGAAAAATGAAGAAACAGGGCTGGATGATTTTGCAGGTCCAATGCAACA  
TCACAGACCCCAACCATGCATAGGAGAGACTCTAACATACTTTAGAGGAGGAGAAAGAGATTC  
CAGTCAAAATTGTCTGCTACCTTTTATGAGCTGTAGGTTCCCTTATTTTATCTTTTTGCTGTG  
GCTTCTAGGAAACACAAAGGTAAAACCCAGATTCCCTATTTTATTTGAGGTTCTTGTTACAATT  
AGCTTTGCCTCACATTTAGCGGTTATGAATCTCATTTTAATATATTCTAACTGTATTATGTTA  
TGAAATCTCTTGGTAAGATAATTTGCATGCTTTCTGGGAGTAGGTAAGGCCTGTGTGCTTGTA  
ATAACTAACATAACTGAAAGTGCAATGTCA

528/615

**FIGURE 524**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108726
><subunit 1 of 1, 686 aa, 1 stop
><MW: 74981, pI: 6.60, NX(S/T): 2
MHARLLGLSALLQAAEQSARLYTVAYYFTTGRLWLWGLALAVLLPGFLVQALSYLWFRAD
GHPGHCSLVMLHLLQLGVWKRHWDAALTSLOKELEAPHRGWLQLQEADLSALRLLEALLQ
TGPHLLLQTYVFLASDFTDIVPGVSTLFSWSSLSWALVSYTRFMGFMKPGHLAMPWAALF
CQQLWRMGMLGTRVLSLVLFYKAYHFWVFVAGAHWLVMTFWLVAQQSDIIDSTCHWRLF
NLLVGAVYILCYLSFWDSPSRNRMVTFYVMMLLENIILLLLATDFLQASWTSLOTIAGV
LSGFLIGSVSLVIYYSLHHPKSTDIWQGLRKSCGIAGGDKTERRDSPRATDLAGKRTES
SGSCQGASYEPTILGKPPTPEQVPPEAGLGTQVAVEDSFLSHHHWLWVKLALKTG NVSKI
NAAFQDN SPAYCPPAWGLSQQDYLRKALSAQQELPSSSRDPSTLENSSAFEGVPKAEAD
PLETSSYVSFASDQQDEAPTQNPAAQTQEGTPEKGA DAVSGTQKG TGGQQRGGEGQQSS
TLYFSATAEVATSSQQEGSPATLQTAHSGRRLGKSSPAQPASPHVGLAPFPDTMADISP
ILGTGPCRGFCPSAGFPGRTLSISELEEPLEPKREL SHHA AVGVVWSLPQLRTAHEPCLT
STPKSESIQTDCSCREQMKQEPSFFI
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-17

**Transmembrane domains:**

Amino acids 35-50;269-287;293-313

**N-glycosylation sites:**

Amino acids 416-420;467-471

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 344-348

**N-myristoylation sites:**Amino acids 188-194;288-294;299-305;335-341;338-344;362-368;  
390-396;473-479;529-535;536-542;558-564;603-609;  
643-649**Amidation sites:**

Amino acids 354-358;568-572

**Leucine zipper pattern:**

Amino acids 112-134

529/615

**FIGURE 525A**

AGTGCCCTCTGTCAATTTAATCTCCACGGAGTCTGAAGGTGCTTCCCAGGTTTGTCCCCATCACACAGATGAGGC  
AATCGTTCTGTAAAGACTGTCCTTGGGTCAATTTATGTTCAGCAATGAAATCGGTGCTGCCATTACTAAACCCCTTACT  
GTGTGCTGGCATTTGTGTATGCATGCATGTGTGTGCGTGCACACGTGTGTGTTTGCCTGTACATGTGCATGTGTGTG  
TTGTGTGCCTGTGTGTGCACATGTAGAAAGAAAGTGATGTGTGGGAATGGAGAATTCCAACCCAGGAGGAGACTG  
TGCTTGGGGCTGCCACGAGAAGTGGTGACACTTCGAGAAACGGGTTCCAAATGCACGTTGCCTTCCAGTTCTCTG  
TGTGACCTTGGGCAAGTCACTTCAGCTCCCTGAGCTTTGTTTTTAAAAATATTTTTTAAATGTATAAAACCATGG  
ACCATTACATATGAAGAGAAATGTGTGTGCAAAACATTCAGTTAATAATCACAGGTGGAGGAGTGCCTGCTCAGA  
CCCAGAGCTGACACAGGGAATCTCCCAGAAGGCTGCAGGGCTTCCCTCCCAACCCCTCCAACGGCCCACTTGCTG  
AGCCCGTGCTTATCTGTTCAGTGGAAATGCCATGTGCCACGTTCCCTCAGAAGTAAAGCCACTAGGTAAGTGTGAC  
ACTCTGTGCCAGCTTGGTGCAAGCCCCCTTGTGTGTGCTATCTTATTGACCTCCCAAATAGCATGGTAAGGTCA  
GTACTGTCACTTCCCCCACTTTGAAGATGAGGAGAGCACAATTCTAGATGGAAATGGAGGTACGCGAGTGGAAA  
TAGGATCCAGACAGATTAATCCAATCTCAAGCCTGAATTTCTTCATTCCACGCTACGCTTGAAGCTCAATCTCTC  
TTCCTGGTTGATTCTCCCCACTTCCCCACCCCAAGATATATCCCATCGCTGCTTGGTGGACAGTACGCTTGGCTG  
GGTTTTGGTAAAGGTGCTGAATAATCAGGCTGCTGGTTAGTTTTTACATTTTACCTTTCCAGTGAATGAGGGC  
CCCATGAAAAGGCGAGCTCAAGTTGTAAATTACTCAAAGGAAGGACAGAAAGGTCTTCTGTTTGCACCTACCTTA  
AGGATTTGGGGTAGACACTGGGAATTTACTAATTTATGAATTCAGTGCTTCCCTTGTGAAAGAGAGGCGTGGAA  
TCAAGCTGAGTGAAGGCATCAAGTTTAAAGTCTAATTAATCTTCTGATCATGCAGAATAAAAGCTACGTCCCTT  
GAAATACACAGCAGCTAAACATAATCTTTCGCTTCCGTAGTGTGGTTAAGGAATCCAGATGTTACTGCAAT  
AACCCTCCATAAAACAAAGGAACACCCAGCTGTGAGAAGTGGCTTCTCAGCATTCGTCAGCAGAGGCTCTTC  
CGGGGCCAGCCCTGGAAGAACCCATCAGGGTCTGATGGTTGCCCTGTTTTCAGCACAGCCCTTATTGGCAGGCAG  
ACGGCTACGGGCACAGCCACAGGCTGAAGGTGAGTCCAGCACACAATTTCTGACAGTGAACAGGAGTAAACATG  
GGACCCACCCGAAACCTTTGTCTGTTGACTTCTTAGCAATGGAGGCAGCTCTAGGCTCTGGAGAGTTCGGGTAT  
AGGAGACCTGACTTGAGCAGACTGATATAAGTGAATGCAACATATTTAGATGGCACAACCTAATTTAGATTT  
ATCAGTGCTAATATAGAAAAGCTAGTATTTTATGGGGCTTATTAGATTTTATAGTCTGAATCCTCACAACCTACG  
AGGGGGTTCGTTTACAGACTATGATCTGTCATGATTTCCCCAAAGATGCTCATTAAGTATATGGTGAAGTAGA  
ATTTGAATACAGAGACCTGGTTCTGCTACTTTCTGTGTTTCTATTGGTTCAAACAGCCTTTCTTCTTTCAA  
ACAATTCAGTGCAATTCATGGTTTTGGAAAATAAACTTGATTTTGAATTCAGACAATAAGTGCATTTTTAATG  
TTTATCTTTTATCTTGA AAAACTGATATATTTATGAATGATATGTGCTCACTCAGTGTCAACACTTCAAACAA  
CACAGACAGTACAATGACAAAATTGGAGATCAGCTCTAATCTCGGCCCAATTTAATGCATTGCTGAATATTCTT  
CTGAACATAGTCCATCCACACTGTCCCATGACACAAGACGCTCCAAGGGGCTGAAGATAGAGGACTTCTGCAG  
TCAAGAGAGCTGGGAACTCTTGGACAGTCAATGTGCATTTGGGTATTAAAGGCTCTGCAAGTTCTGCACCA  
AATAACCCCTTGGATTGGCTTGATCCAATGCCATGTTTCCAAAACCTACTTGCCCGTGGGACACCTTAGTCCATA  
ACACAGGTTGGCATTTCTTCTAGAGAGTGTGCTGTGAAAACACTGGTCTCACAGCACCGTGCATTCATCCAGCA  
GGTATTTTACCAAGCAGGACTTGGGCCAGGTCGCTAGGCTCTGCAGGTGGACAGCCAGCCCTGACCTCCA  
TGGTGTCTCTTCTCATGGGAGAGGCTGCACAGCAGTCAATGAGAAAACGAAGAAACACAGGTAATTTTCAGATG  
CTGATAATGACTACCATGTGCTAAAAGAGCTCCAGGTGTTGCTGTTTTGAGACAATCTTCTCGACAATGAGATA  
GAATGAACCATGCAAACTTTGGGGGCTACGATGGTTTTAGGAAAGAGCTAGAGTGA AAAATCCTTTGACATATAT  
ACATACAAATAAGATACATGTGTATAATTTTATGTAATTGACATCATTATATGCTGGACCTGCCTTTTTTG  
CTTAATGAAAATGTCAAAGGTAATATTACCAATCAATCAATATATTTACCATCGTGTTAATTTCTGCAGAGCA  
CTTATTCAGCACATACTGCATTTTTCTTAGTCACTCACTGGTGGGAATAGAAAAGTTTTCTCAGGCATGCATTTT  
TCCCACTTCTGAAATGATCTCCTTAGAATAAATTTCCCAATTTGATTGCTGGGTTCAAAGGCATGAACATTTTA  
CATTTTTATACAATAATGTCAAACCTTCCGGAATGATGCTCACTTTACTTTCCCTCCAAGACTGTGTGAAA  
ATGCCCATTTTCTAAATGCTTACTATGACTGGTTTTCCAACCTACATTTTAATCTTGTTCATCTGATAGGCAAA  
AAATGATATTTAATTTTTATTTGATTGATAATGACCTTGAACGTGCCATTAGCCTTTTGCATGTATTCTTTTAT  
GAAACATCTGTTTCTATCCTTCGTCAATGTTTCTCATATGTTAACTTTTCTTATTGATTGTTAGAGCACTT  
TGTATATTGTGAATATTAGCTTTTGTGATCAGAATTATGGAATTGTTGTTGCTTTAGTTTTGCTTATCAAGTTT  
AAAGCCATTGAGAGATGTTGTAATGTGTATGTTGTTAAATTTATGTCTTATTTTGTGTTTTCTGATGCTCATAT  
GTTTAGAATGGTCAAGCAATCCCACTTATGATTACATAAATATTCTCCCATATTTGCTCTTAGCATTTTTTTTC  
TTTTCATGTAACCTTTGTTCTTTCAGGAATTTACTTTGCGGTGAGAAATGGGCTGGCTTCCAGTTTTATGTTTC  
CCAAATGGTGATTGAGCTGTTCCATTTCCATATTTCCCTTATTAGAAATGACCACTATATTATGTTCTAAAATA  
TCTGCGTACTTGTGTCCTTCTATAATCTCAGTCACTCTTTGAGCTATCTTTGATTCCTTTTTCAAACCAC  
ACTGCTTTACTGAACTGTATCATCTTATACATTTTTTAACTACAGTCAAGACAAGTTTCTCAATGCCACTCTTTT  
TCAGAGTTTTCTGGTGGTTGTAAGATGTTTATTCTTCTGGATAAACTTTAGAATCACTCTTTTTGTCCAAGGTA  
AAATATATCCACATTGAGATCACTGAATATACAGACTAATTGAGGAAAAATGTATGCTTTTATTGCATTGA  
GTCTTCTTATCCAATAAAAAAGATATGAATTTCCATGTATTGAAATCTTCACTGAGACTTATTTTTGGCTTTTCA



530/615

**FIGURE 525B**

CATGTCCTGCAAATGTATTGTTAAATTTATTTTTAGGTATTTAGGGGAAATGATTTTCTAAAGTTTGTATTTTC  
TAGCTTGTTATAATTTACATATGAGATAGTCATTGTTGTATATTATTTATAACTGATCATATTACTGTATTTGTA  
TTGTTTTAATAGTTTTCTATTATTTTGGGTTTTCCTGGAATACACCTTATTATCTACAAATTATGATTGTTTT  
GCCTTTCCAATGTTTCATAACTGTTTTTATATTCTTGTCTGATTGCTTTGTTTCAGCACTTCTAGAATAAAGTCAT  
GCAATACTAATGA

531/615

**FIGURE 526**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108728
<subunit 1 of 1, 100 aa, 1 stop
<MW: 10922, pI: 8.81, NX(S/T): 0
MSAMKSVLP LLNPYCVLAFVYACMCVRAHVCVCVYMCMCVLCACVCTCRKKVMCGNGEFQ
PRRRLCLGLPREVVTLRETGSKCTLPSSSLCDLGQVTSAP
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-28

**N-myristoylation sites:**

Amino acids 80-86;94-100

**Prokaryotic membrane lipoprotein lipid attachment sites:**

Amino acids 13-24;34-45

532/615

**FIGURE 527**

GTGAGACTTCTTTCTTCATTGTGGCTAGCTTTGAAAAGACCCTCTGAACTTCCTAAAGATATC  
AAGATGATATCACCAGACTTGCCCTTTTTGACAATTGTCTTGATCATAGTTAGTTGGACAACCT  
TGTGGAGCACTAGCCATACTTCTTTCTTATCTTTACTATGTGTTTAAGGTTGTTTCATCTGCAA  
GCCAGCTTAACAACCTTTAAGAATAGCCAGCCTGTGAATCCCAAACACTCTAGAAGAAGTGAA  
AAGAAATCCAATCATCATAAAGACTCCTCAATACACCATCTTCGTTTATCTGCCAACGATGCT  
GAAGATAGCCTTCGCATGCACAGTACTGTGATTAACTTACTAACATGGATTGTATTACTCAGC  
ATGCCTTCTCTAATTTATTGGCTAAAGAATCTTAGGTATTATTTTAACTTAATCCTGATCCA  
TGTAACCTTTGGCATTTATCCTTATTCCGACTATGGCAATTCTTGGAATACTTACACTGTT  
TCAATAAAATCAAGTAAATTGTTGAAGACTACTTCACAATTTCCACTTCCTCTGGCTGTTGGT  
GTGATTGCTTTTGGGTCAGCACATTTATATAGGCTTCCATGCTTTGTCTTCATTCTCTTTTA  
CTCCATGCATTATGCAACTTTATGTAAGATTGGACTTAAGGAATGATGAAGATAATTTATGTG  
TTTAGGGCCAGTGATAAGAGGGAACACACAGATCCATCAGTATGGACAGCAAGATCCTTTGGA  
GAAGACAAGTCTATTTTACAATATTGAAAATAGGAAATTAGTTTGTAAATGTTTGAGGGAAG  
TAGTTGAAGCATGGTTTTGTTTTGTGGTGTGGAATCCATGTACTAATCATTTTGA AAAATTC  
ATGAAGGGATATATGGTGATCACTATCATTGAGGACTCCTGTGCATATAAAATAGTCTGTTTT  
ATCAACTGTAAA

533/615

**FIGURE 528**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108738
><subunit 1 of 1, 196 aa, 1 stop
><MW: 22225, pI: 9.90, NX(S/T): 0
MISPDLPFLTIVLIIVSWTTCGALAILLSYLYYVFKVVHLQASLTTFKNSQPVNPKHSRR
SEKKSNNHHKDSSIHHLRLSANDAEDSLRMHSTVINLLTWIVLLSMPSLIYWLKNLRYYFK
LNPDPCKPLAFILIPTMAILGNTYTVSIKSSKLLKTTSQFPLPLAVGVIAFGSAHLYRLP
CFVFIPLLLHALCNFM
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-25

**Transmembrane domains:**

Amino acids 91-108;128-143;167-186

**N-myristoylation site:**

Amino acids 141-147

534/615

**FIGURE 529**

GCAGAGCCGGGTCCCACCATGGCCGCGAATTATTCCAGTACCAGTACCCGGAGAGAACATGTCA  
AAGTTAAACCAGCTCCCAGCCAGGCTTCCTGGAACGGCTGAGCGAGACCTCGGGTGGGATGT  
TTGTGGGGCTCATGGCCTTCCTGCTCTCCTTCTACCTAATTTTCACCAATGAGGGCCGCGCAT  
TGAAGACGGCAACCTCATTGGCTGAGGGGCTCTCGCTTGTGGTGTCTCCCGACAGCATCCACA  
GTGTGGCTCCGGAGAATGAAGGAAGGCTGGTGCACATCATTGGCGCCTTACGGACATCCAAGCTT  
TTGTCTGATCCAAACTATGGGGTCCATCTTCCGGCTGTGAAACTGCGGAGGCACGTGGAGATG  
TACCAATGGGTAGAAACTGAGGAGTCCAGGGAGTACACCGAGGATGGGCAGGTGAAGAAGGAG  
ACGAGGTATTCCTACAACACTGAATGGAGGTGAGAAATCATCAACAGCAAAAACCTTCGACCGA  
GAGATTGGCCACAAAACCCAGTGCCATGGCAGTGGAGTCATTTCATGGCAACAGCCCCCTTT  
GTCCAAATTGGCAGGTTTTTCCTCTCGTCAGGCCTCATCGACAAAGTCGACAACTTCAAGTCC  
CTGAGCCTATCCAAGCTGGAGGACCCTCATGTGGACATCATTCGCCGTGGAGACTTTTTCTAC  
CACAGCGAAAATCCAAGTATCCAGAGGTGGGAGACTTGCCTGTCTCCTTTCTATGCTGGA  
CTGAGCGGGGATGACCCTGACCTGGGGCCAGCTCAGTGGTCACTGTGATTGCCGGGCAGCGG  
GGTGACCAGCTAGTCCCATTTCTCCACCAAGTCTGGGGATACCTTACTGCTCCTGCACCACGGG  
GACTTCTCAGCAGAGGAGGTGTTTCATAGAGAATAAGGAGCAACTCCATGAAGACCTGGGGC  
CTGCGGGCAGCTGGCTGGATGGCCATGTTTCATGGGCCTCAACCTTATGACACGGATCCTCTAC  
ACCTTGGTGGACTGGTTTTCTGTGTTTCCGAGACCTGGTCAACATTGGCCTGAAAGCCTTTGCC  
TTCTGTGTGGCCACCTCGCTGACCCTGCTGACCGTGGCGGCTGGCTGGCTCTTCTACCGACCC  
CTGTGGGGCCCTCCTCATTGCCGGCCTGGCCCTTGCGCCATCCTTGTTGCTCGGACACGGGTG  
CCAGCCAAAAAGTTGGAGTGAAGAACCCCTGGCACCCGCGGACACCTGCGTGAGCCCTGAGG  
CTGGTTGTACAATGCCACGCGCTGCCTGGCTGCTTTACCTGGGAGTGCTTTTCGATGTGGGCA  
CCTGGGCTTCCTAGGGCTGCTTCTGAGTGGTTCTTTCACGTGTTGTGTCCATAGCTTTAGTCT  
TCCTAAATAAGATCCACCCACACCTAAGTCACAGAATTTCTAAGTTCCCCAACTACTCTCACA  
CCCTTTTAAAGATAAAGTATGTTGTAACCAGGACGTCTTAAATGATTCTTTGTGTACCTTTTC  
TGTCATATTCAGAAACCGTTCTGTGCCTGCTGGGAGTAATTCCTTTAGCAATTAAGTATTTGG  
TAGCTGAATAAGGGGTCAGAACTTCTGAAACCAGAGATCTGTAATCATCTCTATTGGCCTGGG  
GTGCCTGTGCTATAAATGAGTTTCTTCACATGAAAAACACAGCCAGCCCAAGATGACTTATCT  
GGGTTTAGGATTCAATAGTATTCATAACTGCTTATTACATGAGCAATTTTCATCAAATCTCCA  
AACTCTTAAAGGATGCTTTCGGAAAACACGCTGTATACCTAGATGATGACTAAATGCAAAATC  
CTTGGGCTTTGGTTTTTTCTAGTAAGGATTTTAAATAACTGCCGACTTCAAAGTGTCTTA  
AAACGAAAGATAATGTTAAGAAAAATTTGAAAGCTTTGGAAAACCAAATTTGTAATATCATTG  
TATTTTTTATTAAAAGTTTGTAAATAATTTCTAAATTATCA

535/615

**FIGURE 530**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108743
><subunit 1 of 1, 400 aa, 1 stop
><MW: 44876, pI: 8.32, NX(S/T): 2
MAANYSSSTRREHVKVKTSQPGFLERLSETSGGMFVGLMAFLLSFYLIFTNEGRALKT
ATSLAEGLSLVVSPDSIHSVAPENEGRLVHIIGALRTSKLLSDPNYGVHLPVKLRRHVE
MYQWVETEEsREYTEDGQVKKETRYSYNTEWRSEIINSKNFDREIGHKNPSAMAVESFMA
TAPFVQIGRFFLLSSGLIDKVDNFKSLSLSKLEDPHVDIIRRGDFFYHSENPKYPEVGDLR
VSFSYAGLSGDDPDLGPAHVVTVIARQRGDQLVPFSTKSGDTLLLLHHGDFSAAEEVFHRE
LRNSMKTWGLRAAGWMAMFMGLNLMTRILYTLVDWFPVFRDLVNIGLKAFAFVCVATSLT
LLTVAAGWLFYRPLWALLIAGLALVPILVARTRVPAKKLE
```

**Important features of the protein:****Transmembrane domains:**

Amino acids 34-53;365-388

**N-glycosylation site:**

Amino acids 4-8

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 140-144

**Tyrosine kinase phosphorylation sites:**

Amino acids 99-107;220-227

**N-myristoylation sites:**

Amino acids 35-41;93-99;310-316

**Cell attachment sequences:**

Amino acids 221-224;268-271

536/615

**FIGURE 531**

AAAAAAAAAAAAAAAAAGAAGCTCTTATGCCAGGAACCTGGAATGGAGACCAAATATATATTG  
GTTATATCATAGTATCACAGGGTTACTTTGGCATTGTTGGGAACTTGAGAGAAATGGGCAATAA  
CTGTTACTTTAAAAGCTTGGGTGCTGTGATTCTGCCTTCAGCCTCAGCCACTTTTGTGGTGCT  
TTGCGTGGCATCAGTACCTCCACTGATTCTTCTGTCTTTCCTCTCTCTTCCCCCCTCTTT  
CCCTTCTGTTTTTCTCAGATCTAAGGGTTATAATGGAGGGGCAAACTGCCTGGCTATTTTCTCAGA  
TAAGACTTCACTGAGTGACTGTTTCAAGCCATGATTTACCCTGCAGTTTAAACAGGCTCAGGAAT  
TAGGTCGCATCAGTTGAGCGCGGGTCACTTAGGCCTATAATCATCATCAGACGGCAATTAAAG  
GACCATTTCTGCCTTTTTCACTATTACATCCCCGCCTGTAGCCCAGCCTGCCATACAGTAGA  
TACTCAATAAATATTTGCTGAATGATAACCAATAA

537/615

**FIGURE 532**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108758  
<subunit 1 of 1, 100 aa, 1 stop  
<MW: 10316, pI: 8.52, NX(S/T): 0  
MGNNCYFKSLGAVILPSASATFVVLCVASVPPLILLSFLSLFPPSFPSVFLRSKGYNGGA  
NCLAISDKTSLSDCSAHDLPCLTGSGIRSHQLSAGHLGL

**Important features of the protein:****Signal peptide:**

Amino acids 1-47

**N-myristoylation site:**

Amino acids 58-64



538/615

**FIGURE 533**

CGGGGTGTACGAAAGAGAAACCCGGAGGGCGCCGGGGACTGGGCCGGGGTCTGCAGGGGCTCAG  
CTGAGCCCATGAGCTCCCAGAGCTAACCCCTGAACACCCAGGCGGGCAAAGGGCTGATGTCGG  
TAGTCCCCATCCTGGAGGGGACAGGCTCTGCGCATCTGCTCCTGGC**ATGG**CGCTGCGGCACCTC  
GCCCTCCTGGCTGGCCTTCTCGTGGGAGTCGCCAGCAAGTCCATGGAGAACACGGCCCAGCTG  
CCCAGTGCTGTGTGGATGTGGTGGGCGTCAACGCCAGCTGCCAGGCGCAAGTCTGTGTGGT  
CCAGGCTGTTACAGGCGCTGGAACGCGGACGGGAGCGCCAGCTGCGTCCGCTGTGGGAACGGA  
ACCCTCCCAGCCTACAACGGCTCCGAGTGTAGAAGCTTTGCTGGCCCCGGGTGCGCCATTCCCC  
ATGAACAGAAGCTCAGGGACCCCCGGGCGGCCACATCCTGGGGCTCCGCGCGTGGCCGCCTCC  
CTCTTCTGGGCACGTTCTTCATTAGCTCCGGCCTCATCCTCTCCGTAGCTGGGTTCTTCTAC  
CTCAAGCGCTCCAGTAAACTCCCCAGGGCCTGCTACAGAAGAAACAAAGCTCCGGCCCTGCAG  
CCTGGCGAAGCCGCTGCAATGATCCCCCGCCACAGTCTCAGACGTGGGGTCTGCAGGAAAG  
GAGGACCCACCACGACAGGGCAGACCCCCAATACCTGCTCCTCCT**TGA**AGTCCAGCTCCACCC  
GAGGACAGACGACGCGCCCTCCGCCAGGCCCTCCTGAGCAGCCATCGCTTCAGTGGTGCTGG  
GTCAGGCGGACCCAAGAGTCAGCCCGTACGGAAGCCGCGCTACGTCAGGCGGGAGCGGCCCT  
GGACAGGGCCACGGATCCCGCTGCCTTCCCGGGGGAGGCCCGTATCAGCAATGTCTGACCTGG  
AGGCCGAGACCACGCCACGCACTTGGCGGCAGGGACCCGGAGGCCGACCCCTTGGCGGGAACC  
AGCACAAAGTGTTGGCATCGCCCCGGCGCCCGGGACAGTCTGGGCACAGCCTCGGCTCTGGGT  
CCCTCCGCCTCCCAGCGACGGACGCCAAAGGGTCCCGGGCCGCCTGAGGCTCCTCCCCACCAC  
AGCCATCTCGTTTATCGGACCAGGAGCAGGCATCCATGAGACCTCAGAGCTTCAGATCGAGGC  
CTTGGGGGGTCCGGGCCCCCCCCAGGAAACACGGTGAGGCCCCAGCGCCTGCAGCCAAAGCTGG  
CACGATCTATGGGGCAGGTGCCGCTCTGCCTAGAAAAGCCAGGGGCTCTGCTGCCGTGCCCTC  
CAGAGCCACAGCGGGCAGGACTCCTCCAGCACCACCACACCCAGTGGCCCGAGACCCCTCTG  
AGAACAGTGAGGCTGGTCCTCGTGCCGTTCCAGCCGGTGCCCGGCCAGTGGGGAGGACACAGC  
CTAGGAACCAGCTGCCTGAGACCAGGGTGCCTCTGGGCTGTCTCCCGCGTGGCGGAGACCCC  
AAGCACGCAGCCACCCATTTCCGGAGCTGCAGGATAGAGCTTCCTCTTGATCTCTGTTTTTAAG  
CAGAAATTTCATTGTGCAGAAAAGTCCTCCAGAGCTCTGTGGCCCCGCTCGGATCCGCTGGACC  
CCCATGCCTGGCTGATCCCTGCCACGTGGGGCAGGCCACATCTAACCCCCACAAGTCACTG  
CCTCACTGCACCTGCCAAGGCTGCCCTGGCGCTGAGTCTGGGGTCCCTCCCGGAGTTCTTGG  
GAGAAAGGCGCCGTCTGTGGCCGCCTCCCGCACGCCAGGCCCGGGCTCCACCGTGGGTCTCAGA  
CGCCCTGCGGCACCGGCACCGTCTGCTTTAGCATGGGACCCCCATCTGAGGGGTGGCCTGGCC  
TTCGGGGTCCCCACGCTCCTTTGCGAAGTCCACTGTGGGTGCCATCATGGTCTCCGGGACCTG  
GGCCAGCGGGAACGTGGGGGCACTGGGTGTGCTGATATAAAGTCGGCATTACTCAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

539/615

**FIGURE 534**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108765
><subunit 1 of 1, 189 aa, 1 stop
><MW: 19464, pI: 9.60, NX(S/T): 4
MALRHLALLAGLLVGVASKSMентаQLPECCVDVVGVNASCPGASLCGPGCYRRWNADGS
ASCVRCGNGTLPAYNGSECRSFAGPGAPFPMNRSSGTPGRPHPGAPRVAASLFLGTFFIS
SGLILSVAGFFYLKRSSKLPRACYRRNKAPALQPGEAAAMIPPPQSSDVGSAGKEDPPRQ
GRPPIPAPP
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-18

**Transmembrane domain:**

Amino acids 111-129

**N-glycosylation sites:**

Amino acids 38-42;68-72;75-79;92-96

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 134-138

**N-myristoylation sites:**

Amino acids 11-17;36-42;43-49;59-65;69-75;122-128

540/615

**FIGURE 535**

TGGATCTGCGGGAATGTGGGCTGGAGAGGTCCTGCCGTGGTACCAGCCTCCAGCCTGCCCCCA  
GGACTGCCCCCTGACCCAGGCGCGCCCGCTGCTCGGTGGCAGGAGGGCCGGCGGAGCGCC**ATGG**  
CCTGCATCCTGAAGAGAAAGTCTGTGATTGCTGTGAGCTTCATAGCAGCGTTCCTTTTCCTGC  
TGGTTGTGCGTCTTGTAATGAAGTGAATTTCCCATTGCTACTAACTGCTTTGGACAACCTG  
GTACAAAGTGGATAACCATTCCTACACATACAGGCGGCCCTTCGAACTCACTATGGATACA  
TAAATGTGAAGACACAAGAGCCTTTGCAACTGGACTGTGACCTTTGTGCCATAGTGTCAAAC  
CAGGTCAGATGGTTGGCCAGAAGGTGGGAAATGAGATAGATCGATCCTCCTGCATTTGGAGAA  
TGAACAATGCCCCCACCAGGTTATGAAGAAGATGTCGGCCGCATGACCATGATTGAGTTG  
TGTCCTACATACCAGCGTTCCTCTTTTGCTAAAAAACCTGATTATTTTTTCAAGGAAGCGAATA  
CTACTATTTATGTTATTTGGGGACCTTTCCGCAATATGAGGAAAGATGGCAATGGCATCGTTT  
ACAACATGTTGAAAAAGACAGTTGGTATCTATCCGAATGCCCAAATATACGTGACCACAGAGA  
AGCGCATGAGTTACTGTGATGGAGTTTTTAAGAAGGAACTGGGAAGGACAGTACAGAG**TGAC**  
CATGCAGTGTTGATTGATCGAACAGCAACCACCACATACATGTCCTGCCCCACCACAAAAGGA  
AGGAAGGAATAAAAGAAAGAAAGAAAGAAACAAACAAACAAACAAACAAACTAAGCAAGACA  
AAACAAATACCCATGTCAGTGGTTCAAAGATTAAGATTGTGGCTTTGTGTAAAGTTCTTTCCC  
TTTGTAGACTTGCTGCATAATTATTCAGGTATGATGGTTACAGTTTTTAAAAAGGAAGGGAAA  
TTGTGGTATGTGGTATGTAAATATTTTTTAAATGTTGTCTCTCTGTTTGTATCAGTTTTTGTTT  
TATTCAATTTGTCTTTATTAAATCTTATCAAAGCA

541/615

**FIGURE 536**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108783  
><subunit 1 of 1, 210 aa, 1 stop  
><MW: 24022, pI: 9.51, NX(S/T): 1  
MACILKRKSVIAVSFIAAFLFLLVVRLVNEVNFPLLLNCFGQPGTKWIPFSYTYRRPLRT  
HYGYINVKTQEPLQLDCDLCAIVSNSGQMVGQKVGNEIDRSSCIWRMNNAPTKGYEEDVG  
RMTMIRVVSHTSVPLLLKNPDYFFKEANTTIYVIWGPFRNMRKDGNGIVYNMLKKTVGIIY  
PNAQIYVTTEKRMSYCDGVFKKETGKDSTE

**Important features of the protein:****Signal peptide:**

Amino acids 1-27

**N-glycosylation sites:**

Amino acids 148-152

**cAMP- and cGMP-dependent protein kinase phosphorylation sites:**

Amino acids 6-10;191-195;201-205

**N-myristoylation sites:**

Amino acids 41-47;87-93;91-97;167-173;178-184

542/615

**FIGURE 537**

GTTTTATTGACAATACATGCATCATATCTTTTGACTTTGAAGGATATCTCATGTCAAAGGAAT  
CAAGTTATGATTTATAGAGGATTCAGCTGGAATACCTTGTGGGTGCTGGCTGAGGGTGGCAAA  
ACGCCTACCGAGACATGAAGGTTTTAGCCACTAGTTTTGTCCTTGGGAGCCTGGGGTTGGCCT  
TCTACCTGCCTTTGGTGGTGACTACACCTAAAACACTGGCCATCCCTGAGAAGCTGCAAGAAG  
CTGTGGGGAAAGTTATCATCAATGCCACAACCTGTACTGTCACCTGTGGCCTTGGCTATAAGG  
AGGAGACCGTCTGTGAGGTGGGCCCTGATGGAGTGAGAAGGAAATGTCAGACTCAGCGCTTAGAA  
TGTCTGACCAACTGGATCTGTGGGATGCTCCATTTACCATTCTCATTGGCAAGGAATTTGAG  
CTTAGCTGTCTGAGTTCAGACATCTTGGAGTTTGGACAGGAAGCTTTCCGGTTCACCTGGAGA  
CTTGCTCGAGGTGTCATCTCCACTGACGATGAGGTCTTCAAACCCTTTCAAGCCAACTCCCAC  
TTTGTGAAGTTTAAATATGCTCAGGAGTATGACTCTGGGACATATCGCTGTGATGTGCAGCTG  
GTAAAAAAGTTGAGACTTGTCAAGAGGCTCTATTTTGGGTGAGGGTCCTTCCTCCTAACTTG  
GTGAATCTGAATTTCCATCAGTCACTTACTGAGGATCAGAAGTTAATAGATGAGGGATTGGAA  
GTTAATCTGGACAGCTACTCCAAGCCTCACCACCCAAAGTGAAAAAGAAGGTGGCGTCAGCC  
TTGGGAATAGGAATTGCCATTGGAGTGGTTGGTGGCGTGTTGGTGAGGATTGTCCTCTGTGCG  
CTAAGGGGGGGCCTGCAGCAGTGACAGCTTCAAGAACTTAACAGCCTTGCTCCTGAAGAACTG  
GCTGCCCAGGAAGCCAAGCTAGCTTTTTAGGGGAGTGTTCCAGCTGCTGGTAGTGGATCAGCT  
TAGAGGGAACACTCCCACAGCCAAAAGAATGAGTGGGAGAAATGGAGGGGACAATCTCCTGGG  
AGCTATGCGCAGTAACCTAAGTTTCTTATGTCCCATGGATCTCTTCCTGATCTTCCTGCCCA  
TTGGGTACCCAGGAACTGCAAGCATTGCCTGTGTTCTGGGAAGAGTTCTAAGAAGCTTGCA  
TTCATTTTCTACCCTTTATGACTTGGATGCCTCCCCACCTCCATTTCCCTCTTCTGAGCTGT  
GTATTCATGTAGAGGGATGTATTCAGCCTTTTTAGTGAACATTTTTTTTCAATAAAAGTAATT  
CACAGTAA

543/615

**FIGURE 538**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108789  
><subunit 1 of 1, 255 aa, 1 stop  
><MW: 28440, pI: 8.92, NX(S/T): 1  
MKVLATSFVLGSLGLAFYLPVVTPKTLAIPEKLQEAVGKVIINATTCTVTCGLGYKEE  
TVCEVGPDGVRRKCQTQRLECLTNWICGMLHFTILIGKEFELSCLSSDILEFGQEAFT  
WRLARGVISTDDEVFKPFQANSHFVKFYAQEYDSGTYRCDVQLVKNLRLVKRLYFGLRV  
LPPNLVNLNFHQSLTEDQKLIDEGLEVNLDSYKPHHPKWKKKVASALGIGIAIGVVG  
LVRIVLCALRGGLQQ

**Important features of the protein:****Signal peptide:**

Amino acids 1-30

**Transmembrane domain:**

Amino acids 225-244

**N-glycosylation site:**

Amino acids 45-49

**N-myristoylation sites:**

Amino acids 126-132;156-162;204-210;229-235;231-237;235-241

544/615

**FIGURE 539**

CGCTCATCACTGGCTGGGGACAGAGCCGGGCACCAAGGAGCGACAGGATCCCGAAGAGAGAG  
AGAGAAGGCAGCGAGGGAAGGAGGACCCCGGCAGGCAGCAGCATGAAATTCAGCCCAGCGCAC  
TACCTGCTGCCTCTCCTGCCTGCGCTGGTCCTCAGCACCAGACAGGACTATGAAGAGCTAGAA  
AAGCAGCTGAAAGAAGTCTTTAAGGAGCGAAGCACCATTCTTCGTCAGCTGACAAAGACATCA  
AGAGAACTTGATGGAATTAAAGTCAATCTTCAGTCCTTAAAAAACGATGAGCAGTCTGCCAAA  
ACTGATGTTCAGAACTTCTGGAATTAGGACAGAAACAAAGAGAAGAAATGAAGTCTCTTCAG  
GAGGCCCTGCAAAATCAGCTTAAGGAGACATCAGAGAAAGCAGAAAAACACCAGGCTACTATT  
AATTTTTTAAAGACTGAAGTTGAAAGAAAGAGCAAAATGATCCGAGACCTCCAGAATGAGGAT  
TCAAGGAAGAGACCAAGAGATCTCCAGTGGAAGATAGTCTCCATGAGGACCATGTCAATATAC  
TTATTGATGTATCTCTTAGTACCTAGAATAGTGGAGATTTATATTAGATACAAAATAAATATGT  
GTGGAATTAATTAATAA

545/615

**FIGURE 540**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108806
><subunit 1 of 1, 159 aa, 1 stop
><MW: 18865, pI: 9.76, NX(S/T): 0
MKFSPAHYLLPLLPAVLSTRODYEELEKQLKEVFKERSTILRQLTKTSRELDGIKVNLO
SLKNDEQSAKTDVQKLLELGQKQREEMKSLQEALQNQLKETSEKAEKHQATINFLKTEVE
RKSKMIRDLQNEQSRKRPRDLQWKIVSMRTMSIYLLMYL
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-22

**N-myristoylation site:**

Amino acids 54-60



546/615

**FIGURE 541**

CTCCACGAGGCTGCCGGCTTAGGACCCCCAGCTCCGACATGTCGCCCTCTGGTCGCCTGTGTC  
TTCTCACCATCGTTGGCCTGATTCTCCCCACCAGAGGACAGACGTTGAAAGATACCACGTCCA  
GTTCTTCAGCAGACTCAACTATCATGGACATTCAGGTCCCGACACGAGCCCCAGATGCAGTCT  
ACACAGAACTCCAGCCCACCTCTCCAACCCCAACCTGGCCTGCTGATGAAACACCACAACCCC  
AGACCCAGACCCAGCAACTGGAAGGAACGGATGGGCCTCTAGTGACAGATCCAGAGACACACA  
AGAGCACCAAAGCAGCTCATCCCCTGATGACACCACGACGCTCTCTGAGAGACCATCCCCAA  
GCACAGACGTCCAGACAGACCCCCAGACCCTCAAGCCATCTGGTTTTTCATGAGGATGACCCCT  
TCTTCTATGATGAACACACCCTCCGGAAACGGGGGCTGTTGGTCGCAGCTGTGCTGTTTCATCA  
CAGGCATCATCATCCTCACCAGTGGCAAGTGCAGGCAGCTGTCCCGGTTATGCCGGAATCGTT  
GCAGGTGAGTCCATCAGAAACAGGAGCTGACAACCTGCTGGGCACCCGAAGACCAAGCCCCCT  
GCCAGCTCACCGTGCCCAGCCTCCTGCATCCCCTCGAAGAGCCTGGCCAGAGAGGGAAGACAC  
AGATGATGAAGCTGGAGCCAGGGCTGCCGGTCCGAGTCTCCTACCTCCCCCAACCCTGCCCCGCC  
CTGAAGGCTACCTGGCGCCTTGGGGGCTGTCCCTCAAGTTATCTCCTCTGCTAAGACAAAAAG  
TAAAGCACTGTGGTCTTTAAAAA  
AAAAAAAAAAAAAAAAAAAAA

547/615

**FIGURE 542**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108936
><subunit 1 of 1, 178 aa, 1 stop
><MW: 19472, pI: 5.71, NX(S/T): 0
MSPSGRLCLLTIVGLILPTRGQTLKDTTSSSSADSTIMDIQVPTRAPDAVYTELQPTSPT
PTWPADETPQPQTQTQQLEGTDGPLVTDPEETHKSTKAAHPTDDTTLSERPSPSTDVQTD
PQTLKPSGFHEDDPFFYDEHTLRKRGLLVAAVLFITGIIILTSKGCRQLSRLCRNRCR
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-21

**Transmembrane domain:**

Amino acids 147-162

**Tyrosine kinase phosphorylation site:**

Amino acids 45-52

**N-myristoylation site:**

Amino acids 146-152

548/615

**FIGURE 543**

CGGCTCGAGGTGAGAAGGAACTGCAAGAGTGGGGCAGAGAACCAGAGTGTCAGAGCAAAACC  
TCCTCTATCTGCACATCCTGGGGACGAACCGGGCAGCCGGAGAGCTGCGGCCGGCCAGTCCC  
GCTCCGCCTTTGAAGGGTAAAACCCAAGCGGGGCCTTGGTTCTGGCAGAAGGGACGCT**ATGA**  
CCGCAGAATTCCTCTCCCTGCTTTGCCTCGGGCTGTGTCTGGGCTACGAAGATGAGAAAAAGA  
ATGAGAAACCGCCCAAGCCCTCCCTCCACGCCTGGCCCAGCTCGGTGGTTGAAGCCGAGAGCA  
ATGTGACCCTGAAGTGTGAGGCTCATTCACAGAATGTGACATTTGTGCTGCGCAAGGTGAACG  
ACTCTGGGTACAAGCAGGAACAGAGCTCGGCAGAAAACGAAGCTGAATTCCTTCACGGACC  
TGAAGCCTAAGGATGCTGGGAGGTACTTTTGTGCCTACAAGACAACAGCCTCCCATGAGTGGT  
CAGAAAGCAGTGAACACTTGCAGCTGGTGGTCACAGATAAACACGATGAACTGAAGCTCCCT  
CAATGAAAACAGACACCAGAACCATCTTTGTGCGCCATCTTCAGCTGCATCTCCATCCTTCTCC  
TCTTCCTCTCAGTCTTCATCATCTACAGATGCAGCCAGCACGGTTCATCATCTGAGGAATCCA  
CCAAGAGAACCAGCCATTCCAACTTCCGGAGCARGAGGCTGCCGAGGCAGATTTATCCAATA  
TGGAAGGGTATCTCTCTCGACGGCAGACCCCAAGGAGTGACCTATGCTGAGCTAAGCACCA  
GCGCCCTGTCTGAGGCAGCTTCAGACACCACCCAGGAGCCCCCAGGATCTCATGAATATGCGG  
CACTGAAAGTG**TAG**CAAGAAGACAGCCCTGGCCACTAAAGGAGGGGGGATCGTGCTGGCCAAG  
GTTATCGGAAATCTGGAGATGCAGATACTGTGTTTCCTTGCTCTTCGTCCATATCAATAAAAT  
TAAGTTTCTCGTCTTA

549/615

**FIGURE 544**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA119510  
><subunit 1 of 1, 236 aa, 1 stop  
><MW: 26079, pI: 5.05, NX(S/T): 3  
MTAEFLSLLCLGLCLGYEDEKKNEKPPKPSLHAWPSSVVEAESNVTLKCQAHSQNVTFVL  
RKVNDSGYKQEQSSAENAEFPFTDLKPKDAGRYFCAYKTTASHEWSESSEHLQLVVTDK  
HDELEAPSMKTDTRTIFVAIFSCISILLFSLVFIIYRCSQHGSSEESTKRTSHSKLPE  
QEAAEADLSNMERVSLSTADPQGVTYAELSTSALSEAASDTTQEPPGSHEYAALKV

**Important features of the protein:****Signal peptide:**

Amino acids 1-16

**Transmembrane domain:**

Amino acids 135-153

**N-glycosylation sites:**

Amino acids 44-48;55-59;64-68

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 171-175

**Tyrosine kinase phosphorylation sites:**

Amino acids 61-69;87-95

**N-myristoylation sites:**

Amino acids 12-18;203-209

550/615

**FIGURE 545**

GGCGGCCCGGAGCTGGGAGCGCGGGGAAGGCGGTTGGGGTCTGACAGCTGCGCGGATCCTG  
CTCTCTCTCAGCCGCTGTGGACATGCGCAAAGGGCCCTCTCCTGAGTCCAGATGATGCTCAT  
ACCAATGGCTTCAGTGATGGCGGTGACTGAACCGAAATGGGTCTCGGTCTGGAGCCGCTTCCT  
CTGGGTGACGCTGCTGAGCATGGTGCTGGGGTCCCTGCTGGCCCTGCTGCTGCCGCTGGGGGG  
TGTGGAGGAGCAGTGCTTGGCTGTGCTCAAAGGCCTCTACCTGCTCAGGAGCAAACCGGACAG  
GGCGCAGCATGCCGCCACCAAGTGCACCAGCCCGTCCACGGAGCTCAGCATCACCTCCAGGGG  
CGCGACGCTGCTGGTGGCCAAGACCAAGGCCTCTCCAGCGGGTAAGTTGGAAGCCAGAGCTGC  
CCTGAACCAGGCCCTGGAGATGAAGCGCCAGGGCAAGCGGGAAAAAGCCCAAAAGCTCTTCAT  
GCACGCCCTCAAGATGGACCCGGACTTCGTGGACGCGCTCACCGAGTTTGGCATCTTCTCGGA  
AGAAGACAAGGACATCATCCAGGCGGACTACTTGTACACCAGAGCATTGACCATCTCACCTA  
CCATGAGAAAGCACTGGTCAACCGCGATCGGACACTGCCTCTTGTGGAAGAGATCGACCAGAG  
GTATTTTCAGCATCATCGACAGCAAAGTGAAGAAGGTCATGTCCATCCCCAAGGGGAACCTCAGC  
TCTGCGCAGGGTCATGGAGGAGACCTACTACCATCACATCTACCACACAGTGGCCATCGAGGG  
CAACACCCTCACCTCTCGGAAATCAGGCACATCCTGGAGACCCGCTACGCCGTGCCCCGGGAA  
GAGCCTGGAGGAGCAGAACGAGGTCATAGGCATGCATGCAGCCATGAAGTACATCAACACGAC  
TCTGGTTTTCGCGCATCGGCTCCGTACCATCAGCGACGTGCTGGAGATCCACAGGCGGGTGCT  
GGGCTACGTGGACCCCGTGGAAAGCCGGCAGGTTTCGGACAACACAGGTCCTGGTCGGACACCA  
CATCCCTCCCCATCCGCAGGATGTGGAAAAGCAGATGCAGGAGTTTGTACAGTGGCTCAACTCC  
GAGGAAGCCATGAACCTGCACCCAGTGGAGTTTGCAGCCTTAGCCCATTTATAAACTCGTTTAC  
ATCCACCCTTTTCATTGATGGCAACGGGAGGACCTCCCGTCTGCTCATGAACCTCATCCTCATG  
CAGGCGGGCTACCCGCCCATCACCATCCGCAAGGAGCAGCGGTCCGACTACTACCACGTGTTG  
GAAGCTGCCAACGAGGGCGACGTGAGGCCTTTCATTGCTTCATCGCCAAGTGTACTGAGACC  
ACCCTGGACACCCTGCTTTTTGCCACAAGTACTCGGTGGCACTGCCAGAAGCCCAACCC  
AACCCTCTGGGTTCAAGGAGACGCTTCCTGTGAAGCCCTTAACCCTAGAAATCCTCAGTGACA  
AAGGCTGTCCTGAGGTAGGAAA

551/615

**FIGURE 546**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA119517
><subunit 1 of 1, 458 aa, 1 stop
><MW: 51778, pI: 7.81, NX(S/T): 2
MMLIPMASVMAVTEPKWVSWSRFLWVTLLSMVLGSLLALLPLGAVEEQCLAVLKGLYL
LRSKPDRAQHAATKCTSPSTELSITSRGATLLVAKTKASPAGKLEARAALNQALEMKRQG
KREKAQKLFMHALKMDPDFVDALTEFGIFSEEDKDIIQADYLYTRALTISPYHEKALVNR
DRTLPLVEEIDQRYFSIIDSQVKKVMSIPKGNLSALRRVMEETYYHHIYHTVAIEGNTLTL
SEIRHILETRYAVPGKSLEEQNEVIGMHAAMKYINTTLVSRIGSVTISDVLEIHRRVLGY
VDPVEAGRFRTTQVLVGHHPHPQDVEKQMQEFVQWLNSEEAMNLHPVEFAALAHYKLV
YIHPFIDGNGRTSRLMLNLILMQAGYPPITIRKEQQRSDYYHVLEAANEQDVRPFIRFIK
CTETTLDTLLFATTEYSVALPEAQPNHSGFKETLPVKP
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-46

**N-glycosylation sites:**

Amino acids 275-279;446-450

**Tyrosine kinase phosphorylation sites:**

Amino acids 216-225;217-225;244-232

**N-myristoylation sites:**

Amino acids 35-41;235-241;266-272;368-374

**Amidation site:**

Amino acids 119-123

552/615

**FIGURE 547**

CCTCTGTCTGTGCTCCCATCCCAGGGAGTATAGGTGGAGCCTCCAGAGCCCATGGACAGGGCA  
TGCTGGGGCTGGGCCAGCCCCAGCGGTGTCTCTAAGGCACCCCTGGGATCCCCACTGAGCTGG  
CCTACTTCAGACAGCCAGGGCCCCACCCCTCTGGCCCCCTTAGTGTCCAGCTCGTGGCCCCCTTG  
GCATTTCCACAAGACGCCAAGATGGAGATTCCCATGGGGACCCAGGGCTGCTTCTCAAAGAGC  
CTCCTGCTCTCAGCCTCAATCCTGGTCCTCTGGATGCTCCAAGGCTCCCAGGCAGCTCTCTAC  
ATCCAGAAGATTCCAGAGCAGCCTCAAAAGAACCAGGACCTTCTCCTGTCTAGTCCAGGGTGTC  
CCAGACACCTTCCAGGACTTCAACTGGTACCTGGGGGAGGAGACGTACGGAGGCACGAGGCTA  
TTTACCTACATCCCTGGGATACAACGGCCTCAGAGGGATGGCAGTGCCATGGGACAGCGAGAC  
ATCGTGGGCTTCCCCAATGGTTCCATGCTGCTGCGCCGCGCCAGCCTACAGACAGTGGCACC  
TACCAAGTAGCCATTACCATCAACTCTGAATGGACTATGAAGGCCAAGACTGAGGTCCAGGTA  
GCTGAAAAGAATAAGGAGCTGCCCAGTACACACCTGCCACCAACGCTGGGATCCTGGCGGCC  
ACCATCATTGGATCTCTTGCTGCGGGGCCCTTCTCATCAGCTGCATTGCCTATCTCCTGGTG  
ACAAGGAAGTGGAGGGGCCAGAGCCACAGACTGCCTGCTCCGAGGGGCCAGGGATCTCTGTCC  
ATCTTGCTGCTCGGCTGTATCCCCAGTGCCTTCAGTGACGCCCAGCACATGGATGGCGACCACA  
GAGAAGCCAGAATTGGGCCCTGCTCATGATGCTGGTGACAACAACATCTATGAAGTGATGCCC  
TCTCCAGTCCTCCTGGTGTCCCCCATCAGTGACACAAGGTCCATAAACCCAGCCCGGCCCTG  
CCCACACCCCCACACCTGCAGGCGGAGCCAGAGAACCACCAGTACCAGCAGGACCTGCTAAAC  
CCCGACCCTGCCCCCTACTGCCAGCTGGTGCCAACTTCCTGATGGGTCCTGGGCCAGGCCAGC  
CAGGGAGAAGACAAGGCCCCAGCCCTCCTCTGGGAGCCTCACACCTGAGACCAGCAGGACAAG  
GCCATTGGGGGCTGTGGGGCCGATGAGGTGGACTCAGCCAAAGACTCAGCAGCACATGGGGCA  
GGTGTCTGGCAGGGGGACAGGAGACTGTAACAGGCCCCAGGTCCTTGTCAGCCCCCTGAATGC  
ACGCCCCGCTTCGGTCTGTTCCCTCAAGCAAGCTGGCCTGGGCCATGTGCCTGTGAAAGGCAG  
GCTCTGGCCCCCTTCCATGCCAAAGTCCCCCAAGATCTGGATATCTGGGGACAAGATGGTGGC  
CTCAGGCCTGCCTCCCAGGCAGTTGGCTGGGCTCCCAACTGTCTGTCTCAATGCCCTACCCC  
AACTCCACTAGTGACCCTCAGAGTCTTCTCCCCTTAGGACAAGGCAGACACCCCACCATGCGG  
GCCTCAGGTGGCAGAGAGGCCCAGCCTCACAGGCCTGTGGCCCCACACACCAGTCCCAGCAAG  
GTGACCACGGCTGCTGGACCCCTTCCCTGTTTCAGGCAGGCCCAGCCCCCTCTCAGAACCTGCTG  
CCAGCTGCTGGTCTTGGCCCCCACCCTGAATCTTACTGAGTCCCTCTGGGCAGCAGCTCCCTT  
CTCCACCCACCCAGCACCCGTCCCAATGTGGCCTCAGCTTGTCTCCCCTTCCCCAACT  
ATGCATTCAATCAGCAATAAATGAGCCTTTGCTGCA

553/615

**FIGURE 548**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA119535  
><subunit 1 of 1, 300 aa, 1 stop  
><MW: 32638, pI: 6.02, NX(S/T): 1  
MEIPMGTQGCFSKSLLLSASILVWMLQGSQAALYIQKIPEQPQKNQDLLLSVQGVPDF  
QDFNWYLGEETYGGTRLFTYIPGIQRPQRDGSAMGQRDIVGFPNGSMLLRRAQPTDSGT  
QVAITINSEWTMKAKTEVQVAEKNKELPSTHLPNTAGILAATTIIGSLAAGALLISCIAYL  
LVTRNWRGQSHRLPAPRGQGSLSILCSAVSPVPSVTPSTWMATTEKPELGPAGHDAGDNNI  
YEVMPSPVLLVSPISDTRSINPARPLPTPPHLQAEPENHQYQQDLLNPDAPYQCQLVPTS

**Important features of the protein:****Signal peptide:**

Amino acids 1-32

**Transmembrane domain:**

Amino acids 159-178

**N-glycosylation site:**

Amino acids 104-108

**N-myristoylation sites:**

Amino acids 6-12;29-35;55-61;91-97;157-163;165-171



554/615

**FIGURE 549**

GCCACTCACACCATCTGCTAATGGGACAGCTCACTCTTCCCTCCAAACCATGGCCTTGGCTCA  
AGAGCTTCCTTGTTTCTGGAATGTTCTTTCCCTCCAGCTCCAGGTGTTGAAATTCTGCCTGGTC  
TGGGTCTCCTGTTGAAGGACGCCCTCCACTGGGAAGGATCCTCTTGCCTTACCACCTGTCTT  
CACCAGCCCCCTGCTCCCCCTCTTCCCTCTTGGGGCTGTTGTCGTTGTTGATACTTTTTTTTTGTT  
GTGTTTGACACACATCTTCTTCTCACCCCTCTAACACAGTTCTCAACCACAGCACTTTTGTCCC  
TGGAGATGTTGGCAGTGTCCAGAGGCGTGTTGATGGTCCCCTGAGGGTGGGGGTGCTGCTGGCA  
CCAGATGGTAGGGAGATGCCAGGGGTGCTGCTCCACACCCCTATGGGACACTGCACAGTACACC  
TGGCCTGTGTCCCCACAGCGAGAGCTGGCCCTGGGCAGGCGTGGTCCCTGCGGTGTGTGTTG  
GTTGGGATCCTCCACAGTGACAGACGGTGCGCTCTGCCACGTTTCCACACAGCTCTTTTGCT  
TGTGGAGCTACCCCTTTGCAGAGAGCTCATTTCCCTGCGGTCTTTGGCCTGCAGAAGTAAAA  
**TGAGGGGTGGTGAATTACACCCCTGCTGGTTACACATGGAAACTCAGGAGTGAGAATTTTGT**  
GGAGAGCAAGAGAGGTGAGACTGGGGTGCTGGCTGCCAGCCAGGCGGTCCCTCAGCCCCCTGGA  
GAAGCGGGGTGGGGCTGCACACCGAGTCTTCCAGTGAGTCCAGTGATGCTCTCTCCTCTTC  
CTCCCAGTCACCTTTCTCTCCAGTGCCACTACTGCGCTTTCGATGCAGAATAATTCAGTATTT  
GGCGACTTGAAGTCGGACGAGATGGAGCTGCTCTACTCAGCCTACGGAGATGAGACAGGCGTG  
CAGTGTGCGCTGAGCCTGCAGGAGTTTGTGAAGGATGCTGGGAGCTACAGCAAGAAAGTGGTG  
GACGACCTCCTGGACCAGATCACAGGCGGAGACCACTCTAGGACGCTCTTCCAGCTGAAGCAG  
AGAAGAAATGTTCCCATGAAGCCTCCAGATGAAGCCAAGGTTGGGGACACCCTAGGAGACAGC  
AGCAGCTCTGTTCTGGAGTTCATGTGATGAAGTCCTATCCCGACGTTTCTGTGGATATCTCC  
ATGCTCAGCTCTCTGGGGAAGGTGAAGAAGGAGCTGGACCCTGACGACGCCATTTGAACCTTG  
GATGAGACGACGAAGCTCCTGCAGGACCTGCACGAAGCACAGGCGGAGCGCGGCTCTCGG  
CCGTGCTCCAACCTCAGCTCCCTGTCCAACGCCTCCGAGAGGGACCAGCACCCCTGGGAAGC  
CCTTCTCGCCTGAGTGTGCGGGAGCAGCCAGACGTCACCCACGACCCCTATGAGTTTCTTCAG  
TCTCCAGAGCCTGCGGCCTCTGCCAAGACCTAACTCTAGACCACCTTCAGCTCTTTTATTTTA  
TTTTTTTAGTTTTATTTTGCACGTGTAGAGTTTTTGTGTCATCAGACAAGGACTTTGATCCTGTC  
CCCTTTGGCATGCGGGAAGCAGCCGCGGGGAGGTAATGAATTGCTGTGGTATCATGTCAGCA  
GAGTCTCCAAGCCCCACGAACCCTGAGGAGTGGAGTCATACGCGAAGGCCATATGGCCATCGT  
GTCAGCAGAGAGAGTCTCTGTACACAGCCCCGTGAACCCTGAGGAGTGGAGTCATACACGAAG  
GGCGTGTGGCCATCGTGTGACAGAGAGAGTCTCTGTACACAGCCCCGTGAACCCTGAGGAGTGG  
AGTCATACGCGAAGGGTGTGTGGCCAGGCTGCAGAGCTGCGTGCCGTTTGTGTCCGAGCATCA  
CGTGTGGCTCCAGCCCTTGTCTGCCAGTGTAGACACCTCTGTCTGCCCCACTGTCCTGGGG  
TCGCTCTTGGGAGGCACAGGCATGGGTGTGTCTGGCCTCATTCTGTATCAGTCCAGTGTGTTC  
CTGTATAGTTTGTGTCTCCAGGCAGGCCATGGTAGGGGCCTCGCAGGGGCCATTGGGGAGC  
ACAGGGCCAGGCTGGGGTGAGGAGAGCTCCCTGTTTTCTGTTTAATTGATGAGCCTGGGAAA  
GGAGTGTGTTCTGCCTGCCCGTTACAGTGGAGCGTCCGTGTCCATAAAACGTTTTCTAACTG  
GGAA

555/615

**FIGURE 550**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA119537
><subunit 1 of 1, 104 aa, 1 stop
><MW: 11136, pI: 8.20, NX(S/T): 0
MLAVSRGVLMVPLGLGVLLAPDGREMPGVLLHTLWDTAQYTWPVSPPTARAGPGQAWSLRC
VLVGILHSDRRRCALPTFPHSSFACGAHPFAESSFPCGLWPAEVK
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-20

**N-myristoylation sites:**

Amino acids 53-59;64-70;97-103

**Prokaryotic membrane lipoprotein lipid attachment site:**

Amino acids 74-85

556/615

**FIGURE 551**

CGCCCTTAGCATGGGTTTCTGCCGAGCGCCCTGCACCCGCTGTCTCTCCTGGTGCAGGCCATCATGCTGGCCAT  
GACCCTGGCCCTGGGTACCTTGCCTGCCTTCTACCCTGTGAGCTCCAGCCCCACGGCCTGGTGAAGTGAAGTGA  
GCTGTTCTTGAAGTCTGTGCCCCACTTCTCCATGGCAGCACCCCGTGGCAATGTCACCAGCCTTTCTTGTCTCTC  
CAACCGCATCCACCACCTCCATGATTCTGACTTTGCCACCTGCCAGCCTGCGGCATCTCAACCTCAAGTGGAA  
CTGCCCGCCGTTGGCCTCAGCCCCATGCACCTCCCCTGCCACATGACCATCGAGCCCAGCACCTTCTTGGCTGT  
GCCACCCCTGGAGAGCTAAACCTGAGCTACAACAACATCATGACTGTGCCTGCGCTGCCAAATCCCTCATATC  
CCTGTCCCTCAGCCATACCAACATCCTGATGCTAGACTCTGCCAGCCTCGCCGGCCTGCATGCCCTGCGCTTCT  
ATTATGAGCGCAACTGTTATTACAAGAACCCTGCAGGCAGGCACTGGAGGTGGCCCCGGGTGCCCTCCTTGG  
CCTGGGCAGCCTCACCCACCTGTCACTCAAGTACAACAACCTCACTGTGGTGGCCGCAACCTGCCTTCCAGCCT  
GGAGTATCTGCTGTTGTCTTACAACCGCATCGTCAAACCTGGCGCCTGAGGACCTGGCCAATCTGACCGCCCTGCG  
TGTGCTCGATGTGGGCGGAAATTGCCGCGCTGCGACCAGCTCCCAACCCCTGCATGGAGTGCCTTCGTCACTT  
CCCCAGCTACATCCCGATACCTTCAGCCACCTGAGCCGTCTTGAAGGCTGGTGTGAAGGACAGTTCTCTCTC  
CTGGTGAATGCCAGTTGGTTCCGTGGGCTGGGAAACCTCCGAGTGTGACCTGAGTGAAGTCTCTCTACAA  
ATGCATCACTAAAACCAAGGCCCTCCAGGGCCTAACACAGCTGCGCAAGCTTAACCTGTCTTCAATTACCAAAA  
GAGGGTGTCTTTGCCACCTGTCTCTGGCCCCCTTCTTGGGAGCCTGGTGGCCCTGAAGGAGCTGGACATGCA  
CGGCATCTTCTCCGCTCACTCGATGAGACCAGCTCCGGCCACTGGCCCGCCTGCCATGCTCCAGACTCTGCG  
TCTGCAGATGAACCTTCAACAACAGGCCAGCTCGGCATCTTCAGGGCCTTCCCTGGCCTGCGCTACGTGGACCT  
GTCGGACAACCGCATCAGCGGAGCTTTCGGAGCTGACAGCCACCTGAGGGGAGGAGATGGAGGGGAGAAGGTCTG  
GCTGCAGCCTGGGACCTTGTCTCCGGCCCCAGTGGACACTCCCAGCTCTGAAGACTTCAGGCCAACTGCAGCAC  
CCTCAACTTCACCTTGGATCTGTACGGAACAACCTGGTGACCGTGCAGCCGGAGATGTTTGGCCAGCTCTCGCA  
CCTGCAGTGCCTGCGCCTGAGCCACAACCTGCATCTCGCAGGCACTCAATGGCTCCAGTTCTGCGCCTGACCGG  
TCTGCAGGTGTAGACCTGTCCACAATAAGCTGGACCTCTACCAGGAGCACTCATTACGGAGCTACCACGACT  
GGAGGCCCTGGACCTCAGCTACAACAGCCAGCCCTTTGGCATGAGGGCCTGGGGCCACAACCTTCAGCTTCTGTCG  
TCACCTGCGCACCCCTGCGCCACCTCAGCCTGGCCCAACAACATCCACAGCCAAGTGTCCAGCAGCTCTGCAG  
TACGTCGCTGCGGGCCCTGGACTTCAGCGGCAATGCACTGGGCCATATGTGGGCCGAGGGAGACCTCTATCTGCA  
CTTCTTCCAAGGCCTGAGCGGTTTGTATCTGGCTGGACTTGTCCAGAACCGCCTGCACACCCTCCTGCCCAAAC  
CCTGCGCAACCTCCCCAAGAGCCTACAGGTGCTGCGTCTCCGTGACAATTACCTGGCCTTCTTTAAGTGGTGGAG  
CCTCCACTTCTTGCCCAAACCTGGAAGTCTCGACCTGGCAGGAAACAGCTGAAGGCCCTGACCAATGGCAGCCT  
GCCTGCTGGCACCCGGCTCCGGAGGCTGGATGTGAGCTGCAACAGCATCAGCTTCTGTCGCCCCGGCTTCTTTT  
CAAGGCCAAGGAGCTGCGAGAGCTCAACCTTAGCGCCAACGCCCTCAAGACAGTGGACCACTCCTGGTTTGGGCC  
CCTGGCGAGTGGCCTGCAATACTAGATGTAAGCGCCAACCCCTCTGCACTGCGCCTGTGGGGCGGCCTTTATGGA  
CTTCTGCTGGAGGTGCAGGCTGCCGTGCCCGGTCTGCCAGCCGGGTGAAGTGTGGCAGTCCGGGGCCAGCTCCA  
GGGCCTCAGCATCTTTGCACAGGACCTGCGCCTCTGCTGGATGAGGCCCTCTCCTGGGACTGTTTCGCCCCCTC  
GCTGCTGGCTGTGGCTCTGGGCCTGGGTGTGCCATGCTGCATCACCTCTGTGGCTGGGACCTCTGGTACTGCTT  
CCACCTGTGCTGGCCTGGCTTCCCTGGCGGGGGCGGCAAGTGGGCGAGATGAGGATGCCCTGCCCTACGATGC  
CTTCGTGGTCTTCGACAAAACGAGAGCGCAGTGGCAGACTGGGTGTACAACGAGCTTCGGGGGCGAGCTGGAGGA  
GTGCCGTGGGGCCTGGGCACTCCGCTGTGCTGGAGGAACCGGACTGGCTGCCGGCAAAACCCCTCTTTGAGAA  
CCTGTGGGCCTCGGTCTATGGCAGCCGCAAGACGCTGTTTGTGCTGGCCACACGGACCGGGTCACTGGTCTCTT  
GCGCGCCAGCTTCTGTGTCGCCCAGCAGCGCCTGCTGGAGGACCGCAAGGACGTCGTGGTGTGCTGATCCTGAG  
CCCTGACGGCCGCGCTCCCGCTACGTGCGGCTGCGCCAGCGCCTTCTGCCGCAAGTGTCTCTCTGTCGCCCCA  
CCAGCCCAGTGGTCAAGCAGCTTCTGGGCCAGCTGGGCATGGCCCTGACCAGGGACAACCACTTCTATAA  
CCGGAACCTTCTGCCAGGGACCCACGGCCGAATAGCCGTGAGCCGGAATCCTGCACGGTGCCACCTC

557/615

**FIGURE 552**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA119714  
><subunit 1 of 1, 1032 aa, 1 stop  
><MW: 115799, pI: 8.61, NX(S/T): 12  
MGFCRSALHPLSLLVQAIMLAMTLALGTLPAFLPCELPQPHGLVNCNWLFLKSVPFHFSMAA  
PRGNVTSLSLSSNRIHHLHDSDFAHLPSLRHLNLKWNCPVGLSPMHFPCHMTIEPSTFL  
AVPTLEELNLSYNNIMTVPALPKSLISLSLSHTNILMLDSASLAGLHALRFLFMDGNCY  
KNPCRQALEVAPGALLGLGSLTHLSLKYNNTLVVPRNLPSSLEYLLLSYNRIVKLAPEDL  
ANLTALRVLDVGGNCRCDHAPNPCMECPRHFPQLHPDTFSHLSRLEGLVLKDSLSLWLN  
ASWFRGLGNLRVLDLSENFYKCIKTALQGLTQLRKLNLSENYQKRVSAHLSLAPSF  
GSLVALKELDMHGIFFRSLDETTLRPLARLPMQLTLRLQMNFINQAQLGIFRAFPGLRYV  
DLSDNRISGASELTATMGEADGGEKVWLQPGDLAPAPVDTPSSEDFRPNCSTLNFTLDLS  
RNNLVTVQPEMFAQLSHLQCLRLSHNCISQAVNGSQFLPLTGLQVLDLSHNKLDLYEHS  
FTELPRLALDLSYNSQPFQGMQGVGHNFSAHLRTRLRHLSLAHNNIHSQVSQQLCSTSL  
RALDFSGNALGHMWAEGDLYLHFFQGLSGLIWLDSLQNRLHTLLPQTLRNLPKSLQVLR  
RDNYLAFFKWWSLHFLPKLEVLDLAGNQLKALTNGSLPAGTRLRRLDVSCNSISFVAPGF  
FSKAKELRELNLSANALKTVDSWFGPLASALQILDVSANPLHCACGAAFMDFLELVQAA  
VPGLPSRVKCGSPGQLQGLSIFAQDLRLCLDEALSWDCFALSLLAVALGLGVPMHLHLCG  
WDLWYCFHLCLAWLPWRGRQSGRDEDALPYDAFVVFDKTQSAVADWVYNELRGQLEECRG  
RWALRLCLEERDWPGLKTLFENLWASVYGSRKTLFVLAHTDRVSGLLRASFLLAQQRLLE  
DRKDVVVLVILSPDGRRSRYVRLRQRLCRQSVLLWPHQPSGQRSFWAQLGMALTRDNHFF  
YNRNFCQGPTAE

**Important features of the protein:****Signal peptide:**

Amino acids 1-30

**Transmembrane domain:**

Amino acids 818-835

**N-glycosylation sites:**Amino acids 64-68;129-133;210-214;242-246;300-304;340-344;  
469-473;474-477;513-517;567-571;694-698;731-735**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 347-351

**Tyrosine kinase phosphorylation site:**

Amino acids 863-871

**N-myristoylation sites:**Amino acids 27-33;41-47;63-69;193-199;361-367;409-415;  
563-569;607-613;695-701;794-800;929-935;945-951;  
1010-1016**Amidation site:**

Amino Acids 974-978

**Leucine zipper patterns:**

Amino acids 204-226;644-666;814-836

558/615

**FIGURE 553**

GGCGTGGGACGTGCTGCGGCGTCCTAGCTGGCTTACAGGGCGGCGGGGGTGTGTGTCCTCT  
GTTAAGAGTGCTACTCGCCCGGGGTGATCTGTGCATGCCACTCCTGGGTGAGACGGTGAGGT  
CGGCGTCTGCGAGGACGCGGCGGTGGAGTAGAAGGGCAGCCGGAGACAGGCCCGGCGCCCTT  
CCGAGGCTAGACGGCCCCAGCTTCGCGGGGATCATGGCCATTGCTGGTGGACCGAGTGCGGGGC  
CACTGGCGAATCGCCGCCGGGCTCCTGTTCAACCTGCTGGTGTCCATCTGCATTGTGTTCCCTC  
AACAAATGGATTTATGTGTACCACGGCTTCCCCAACATGAGCCTGACCCTGGTGCACCTTCGTG  
GTCACCTGGCTGGGCTTGTATATCTGCCAGAAGCTGGACATCTTTGCCCCAAAAGTCTGCCG  
CCCTCCAGGCTCCTCCTCCTGGCCCTCAGCTTCTGTGGCTTTGTGGTCTTCACTAACCTTTCT  
CTGCAGAACAAACACCATAGGCACCTATCAGCTGGCCAAGGCCATGACCACGCCGGTGATCATA  
GCCATCCAGACCTTCTGCTACCAGAAAACCTTCTCCACCAGAATCCAGCTCACGCTGATTCCCT  
ATAACTTTAGGTGTAATCCTAAATTCTTATTACGATGTGAAGTTTAATTTCTTGGAATGGTG  
TTTGCTGCTCTTGGTGTTTTAGTTACATCCCTTTATCAAGTGTGGGTAGGAGCCAAACAGCAT  
GAATTACAAGTGAATCAATGCAGCTGCTGTACTACCAGGCTCCGATGTCATCTGCCATGTTG  
CTGGTTGCTGTGCCCTTCTTTGAGCCAGTGTTTGGAGAAGGAGGAATATTTGGTCCCTGGTCA  
GTTTCTGCTTTGCTTATGGTGCTGCTATCTGGAGTAATAGCTTTCATGGTGAACCTTATCAATT  
TATTGGATCATTGGGAACACTTCACCTGTCACCTATAACATGTTCCGACACTTCAAGTTCTGC  
ATTACTTTATTTCGGAGGATATGTTTTATTTAAGGATCCACTGTCCATTAATCAGGCCCTTGGC  
ATTTTATGTACATTATTTGGCATTCTCGCCTATACCCACTTTAAGCTCAGTGAACAGGAAGGA  
AGTAGGAGTAACTGGCACAACGTCCTTAATTGGGTTTTTGTGGAGAAAAGAATGTTGTCCCA  
AGAAGATAAAAAATATTGTTAAGTGTGCAAGTTATTA

559/615

**FIGURE 554**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA125170
><subunit 1 of 1, 313 aa, 1 stop
><MW: 35066, pI: 9.39, NX(S/T): 5
MALLVDRVRGHWRIAAGLLFNLLVSICIVFLNKWIYVYHGFPNMSLTLVHFVVTWLGLYI
CQKLDIFAPKSLPPSRLLLLALSFCGFVVFTNLSLQNNTIGTYQLAKAMTTPVIIAIQTF
CYQKTFSTRIQLTLIPITLGVILNSYYDVKFNFLGMVFAALGVLVTSLYQVWVGAKQHEL
QVNSMQLLYYQAPMSSAMLLVAVPFFEPVFGEGGIFGPWSVSALLMVLLSGVIAFMVNLS
IYWIIGNTSPVTYNMFHFKFCITLFGGYVLFKDPLSINQALGILCTLFGILAYTHFKLS
EQEGSRSKLAQRP
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-27

**Transmembrane domains:**

Amino acids 46-60;75-90;153-167;192-208;221-237

**N-glycosylation sites:**

Amino acids 43-47;92-96;97-101;238-242

**N-myristoylation sites:**

Amino acids 17-23;57-63;140-146;155-161;162-168;283-289

560/615

**FIGURE 555**

GTTAGGCAGAGCCAAGGTGGTTGCAGACCTGGAATCAGAACAGCTTTTAGACCAACCTGAAAG  
CAGGAATGTAAGCACTGTTACAGAGATTTTCGTCTTTGGCTTATTGTGCCTGCAGAGTCTAG  
TGCTTCTTTGCCAGCTGTGCTGACTCAGCACTCCATGCCTGTTTTCTGGAACCACTCCCTGGA  
GCTGGGCCATGTTTTGATTGACAGTGTGGAGCTAGCCCAGCAAGTACTCTACATGCAACCCCC  
CAGCCAGGCACTACCTCTGCTCCTCCTCCATGGCCTCCTGCTACACCGGCAGCTCTATGGAAC  
AAGGCTGCAGGCACACAGGGGGCGCTGGAGTCAAGTGAAGTCTAAGCCAGGTTCTTCAGACCCA  
AGACCAGCTGTGGGCAAGTCTTAGCAATCCCCGTGCTGCCATGCAAGAGCTGGCTGCTTCAGT  
TTTCTACGGGGGTCTCTGGGGGACACTGAGGACAGGGAGGCCCTGATTAGCCTCACACAAGC  
CTGCCTGAGCCCCAGTAGTGGGAGCTGGGTCCAGCCACACACACCTCAGTCTTTGCTGGCCAC  
GCTCATGCCCCCTCCAGCTAAGGGAGCTGGATGCAATGGCAGAGTGCAAGGCCCAAGATGCACC  
TACTGCCCTCACCACCTGAACCCCCGGCTCTGCGGACTGAGTGAGGGCCCCCAAGCCTGGCTGT  
TGCGACGCCAGAGTCGCGCTCTCTTGAGTGCCTGTCAGCGGAGTTCACCCGTGTGGGTCTCTG  
AGTCTCGAAGAGGCGCCAGCTTGCGGAAAGGCGACTGCGGCAACGCCTAGTGCAAGTCAACCG  
GAGGCTGGAGTCACTGCAGGATCTGCTGACCCACGTGATTGCGCAAGACGAGTCCGACGCCCC  
GTGGTCAGTGCTGGGGCCAAATGCACGGCGGCCCTCTGGAGGGCGTCTTAGAGACCGAGGCTCT  
AGAACTGAGCCAGTTGGTGGGCACGCTACAACGCGACCTTGATTGCCTGTTGCAGCAGCTGAA  
GGGCGCACCCCCGTGCCCCCTCCGCGCTGTGCTGCGGTGGCCACGCTCTCTGGACTGGCCG  
CCTACCCTTGCCCTTGCGGACCTCATGCGCCGGCCGGTCCGCAGCCGCCCTGGCACTGGCTGCG  
ACAGTTGTGCGCGCCGTGGGCAACTGTTGGTTTCGTTACTTGGGCGTGGGCGCGGACGCGAGCAG  
TGATGTACCAGAGCGCGTCTTCCACCTGTCAGCCTTTCGCCACCCGCGCCGCTGCTGCTGGC  
ATTGCGTGGGGAAGCTGCCCTGGACCAGAATGTGCCAGCTCGAATTTCCCTGGTAGCCGAGG  
CTCGGTCTCCAGTCAGCTCCAGTATAAACGTCTGGAGATGAACAGCAACCCCTCTGCACTTCAG  
GGTGGAGAATGGTCCAAATCCCACGGTTCCAGAGAGAGGGCTGCTGCTGATCGGGCTACAGGT  
CCTACATGCGGAGTGGGACCCAATAGCTGGAGCCTTGAGGACAGTCCTTCCAGCCAACCCAG  
CCCTCTGCCTCCCGTCAGCATCAGCACACAGGCCCGGGCACCAGTGACCTGCCAGCCCCAGC  
CGACCTGACTGTGTACTCGTGTCTGTGTACATGGGAGGGCCCCCTTGGCACCGCTAAGCTGCA  
GAGCAGGAACATCGTGATGCATCTGCCCTTACCCACCAAGCTCACCCCCAACACCTGTGTCCA  
AAGGAGGGTCCATGTGTGCAGCCACCCCTGTCTTGAGCCCGTCTACCAAAATAAAGTTGTAG  
TGATTCCA

561/615

**FIGURE 556**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA129594
><subunit 1 of 1, 162 aa, 1 stop
><MW: 17598, pI: 6.58, NX(S/T): 1
MPVFWNQSLELGHVLI DSVELAQQVLYMQPPTQALPLLLHGLLLHRQLYGTRLQAHGR
WSQVTLTQVLQTQDQLWASLSNPRAAMQELAASVFYGGPLGDTEDREALISLTQACLSPS
SGSWVQPHTPQSLLATLMPLPAKGAGCNGRVQGPDPAPTALT
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-45

**N-glycosylation site:**

Amino acids 6-10

**N-myristoylation sites:**

Amino acids 97-103;144-150



562/615

**FIGURE 557**

GACCTTGAGCCCTCGAAAGCGACATGGCGGTTCTCTTAAAGCTGGGCGTTCTCTGCAGTGGCC  
AAGGAGCTCGAGCTCTCCTACTCCGAAGCCGGGTGGTCAGACCCGCTTATGTGTGAGCATTTC  
TCCAGGACCAGCCTACCCAAGGACGGTGTGGTACCCAGCACATTACCTGTCACCAAGCCACC  
ACTCTGGTTCCAAGGCTGCATCTCTCCACTGGACCAGTGAGAGGGTTGTCAGTGTTCTGCTCT  
TGGGGCTGATCCCTGCTGGGTACTTGAATCCCTGCTCTGTGGTGGACTACTCTCTGGCTGCAG  
CCCTCACCCCTGCACAGTCACTGGGGCCTTGGACAAGTGGTTACCGACTACGTTTCATGGGGACA  
CCCTGCCGAAGGCTGCCAGGGCAGGCCTCTTGGCACTCTCAGCTTTGACCTTTGCTGGGCTTTGC  
TACTTCAATTACCACGATGTCGGCATCTGCAGAGCGGTTGCCATGCTGTGGAAGCTCTTGACTT  
GGGTGCAGCACTTTGATTGTGTGCCTCCTTGCCTCTGCTTTACCAATGCCGTTACCTCGCAG  
TGAGGGGGGATGAAGGATAAGCCCATTGGTGGGCAGAATGTCTTCTAATTACATGGTTATTTT  
CAGAATTTATTTGTTGAGGAAGAGGTTTGAGGAGTTAGGTTGACCATTCGTGAGTCTGTGTT  
CCATACTCCACTGAGTGTGGGCCTAGCTCACAGCCTCGCGGTGAGACTGAACATTTTCATGAG  
CTCATGTTGCCTTTGACCACCATTTCTTAAGGAGAGCCAGCTGATTGCTGTCAGGATAAGAGC  
ATCTCTTCAGCCAGGAGGGAGGCCTGTTCCCTCCTGAGTTAGACTTTGCATGAAGCTCGAAAG  
TATTCCCTTTGGAACCTCCCATTTCTTGTTCAGGTGACACCAGCTCTGTTGATGGCTCTGCTTC  
TAGGGAACATTTAATCAGGAGATGCTCTCAATGACTAATTTGTCTAAGTCTTAGGAAGGAGGT  
TGAGGAAAGCTGGATTTAGACAAGTTCAATTTAGGGAGTTCTCCTTGTTTGTGGATTAAAATA  
TGACAGATTGCAAACAGACTACTCTTCAAATGTATCTCAATTGTGCAGAAGTGAGCTGTCCAA  
AAGTATAAGACTAAGTGATAAACTGTCTTCCACCGTGGGAGTTGTTAATGAGAAAGAAAGTG  
TACTCTGAAAAACAAGGGGG

563/615

**FIGURE 558**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA129793
><subunit 1 of 1, 159 aa, 1 stop
><MW: 17014, pI: 9.38, NX(S/T): 0
MAVLLKLGVLCSGQGARALLRSRVVRPAYVSAFLQDQPTQGRCGTQHIHLSPSHHSGSK
AASLHWTSERVVSLLLLGLIPAGYLNPCSVVDYSLAAALTLHSHWGLGQVVTDYVHGDTL
PKAARAGLLALSALTFAGLCYFNYHDVGICRAVAMLWKL
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-15

**Transmembrane domains:**

Amino acids 71-88;126-140

**Glycosaminoglycan attachment site:**

Amino acids 12-16

**N-myristoylation sites**

Amino acids 8-14;58-64;78-84;108-114;148-154

564/615

**FIGURE 559**

CCCAGCCCCGCGTTTCGGCTGCTCTCGAGGAGGCCGGAGTCCCCGGAGACGATGCGCCCCGCGC  
AGCCGCCTGCGCCTGCGGGAGCCGGCTGCCCTTGAGATGGAGTTGCTGCCTCTTTGGCTCTGC  
CTGGGTTTTTCACTTCCTGACCGTGGGCTGGAGGAACAGAAAGCGGAACAGCCACAGCAGCCTCC  
CAAGGAGTCTGCAAGTTGGTGGGTGGAGCCGCTGACTGCCGAGGGCAGAGCCTCGCTTCGGTG  
CCCAGCAGCCTCCCGCCCCACGCCCGGATGCTCACCCCTGGATGCCAACCCCTCTCAAGACCCTG  
TGGAATCACTCCCTCCAGCCTTACCCTCTCCTGGAGAGCCTCAGCCTGCACAGCTGCCACCTG  
GAGCGCATCAGCCGCGGCGCCTTCCAGGAGCAAGGTCACCTGCGCAGCCTGGTCCTGGGGGAC  
AACTGCCTCTCAGAGAACTACGAAGAGACGGCAGCCGCCCTCCACGCCCTGCCGGGCCTGCGG  
AGGCTGGACTTGTGAGGAAACGCCCTGACGGAGGACATGGCAGCGCTCATGCTCCAGAACCCTC  
TCCTCGCTGCGGTCCGTGTCCCTGGCGGGGAACACCATCATGCGGCTGGACGACTCCGTCTTC  
GAGGGCCTGGAGCGTCTCCGGGAGCTGGATCTGCAGAGGAACTACATCTTCGAGATCGAGGGC  
GGCGCTTTCGACGGCCTGGCTGAGCTGAGGCACCTCAACCTGGCCTTCAACAACCTCCCCTGC  
ATCGTGGACTTCGGGCTCACGCGGCTGCGGGTCCTCAACGTGAGCTACAACGTCTGGAGTGG  
TTCCTCGCGACCGGGGGAGAGGCTGCCTTCGAGCTGGAGACGCTGGACCTGTCTCACAACCAG  
CTGCTGTTCTTCCCGCTGCTGCCCCAGTACAGCAAGTTGCGGACCCTCCTGCTGCGCGACAAC  
AACATGGGCTTCTACCGGGACCTGTACAACACCTCGTCGCCGAGGGAGATGGTGGCCCAGTTC  
CTCCTCGTGGACGGCAACGTGACCAACATCACCACCGTCAGCCTCTGGGAAGAATTCTCCTCC  
AGCGACCTCGCAGATCTCCGCTTCCTGGACATGAGCCAGAACCAGTTCAGTACCTGCCAGAC  
GGCTTCCTGAGGAAAATGCCTTCCCTCTCCCACCTGAACCTCCACCAGAATTGCCTGATGACG  
CTTCACATTCGGGAGCACGAGCCCCCGGAGCGCTCACCGAGCTGGACCTGAGCCACAACCAG  
CTGTGCGGAGCTGCACCTGGCTCCGGGGCTGGCCAGCTGCCTGGGCAGCCTGCGCTTGTTCAAC  
CTGAGCTCCAACCAGCTCCTGGGCGTCCCCCTGGCCTCTTCGCCAATGCTAGGAACATCACTAC  
ACTTGACATGAGCCACAATCAGATCTCACTTTGTCCCTGCCAGCTGCCTCGGACCGGGTGGG  
CCCCCTAGCTGTGTGGATTTTCAAGGAATATGGCATCTTTAAGGAGCCTGTCTCTGGAGGGCTG  
TGGCCTGGGGGCATTGCCAGACTGCCCATTTCCAAGGGACCTCCCTGACCTACTTAGACCTCTC  
AAGCAACTGGGGGGTTCTGAATGGGAGCCTCGCCCCACTCCAGGATGTGCCCCCATGTTACA  
GGTCTGTCTCTCAGGAACATGGGCCTCCACTCCAGCTTTATGGCGTTGGACTTCTCTGGGTT  
TGGGAATCTCAGGGACTTAGATCTGTGCGGGAATTGCTTGACCACCTTCCAAGGTTTGGGGG  
CAGCCTGGCCCTGGAGACCCTGGATCTCCGTAGAACTCGCTCACAGCCCTTCCCCAGAAGGC  
TGTGTCTGAGCAGCTCTCGAGAGGTCTGCGGACCATCTACCTCAGTCAGAATCCATATGACTG  
CTGTGGGGTGGATGGCTGGGGGGCCCTGCAGCATGGGCAGACGGTGGCCGACTGGGCCATGGT  
CACCTGCAACCTCTCCTCCAAGATCATCCGCGTGACGGAGCTGCCCGGAGGTGTGCCTCGGGA  
CTGCAAGTGGGAGCGGCTGGACCTGGGCCTGCTCTACCTCGTGCTCATCCTCCCCAGCTGCCT  
CACCTGCTGGTGGCCTGCACTGTATCGTCCTCACTTTTAAGAAGCCTCTGCTTCAGGTCAT  
CAAGAGCCGCTGCCACTGGTCCCTCCGTTTACTGACCTGGCTGTGTGCCAAGACTCGAAATTCTG  
GTCCGCACACAACAGGACACTTTCTCTGCCAGCTTTCAAGATGTGATGCAGAGGCCAAGTCTG  
ACGAATTGAAGTTTCAATTAAAATTTAATATGTTTCCATTCTCATCGCCACCCCCACCCCG  
CCCCACCACCGCCCAAGTTCTTTTCCATCATTATAATTATCCTTATTATCTTGGTAAAAT  
ATTTATTAAGTGACTTTTTCAGAAATAAAAGGCAACGTGTCTCATAAATATTTTTTAAAAAA  
AAAAAAAAAAAAA

565/615

**FIGURE 560**

><subunit 1 of 1, 692 aa, 1 stop  
><MW: 76366, pI: 6.07, NX(S/T): 11  
MELLPLWLCLGFHFLTVGWRNRSGTATAASQGVCKLVGGAADCRGQSLASVPSSLPPHAR  
MLTLDANPLKTLWNHSLQPYPLLESLSLHSCHLERISRGAFQEQGHLRSLVLGDNCLSEN  
YEETAAALHALPGLRRDLDSGNALTEDMAALMLQNLSSLRSVSLAGNTIMRLDDSVFEG  
ERLRELDLQARNYIFEIEGGAFDGLAELRHLNLAFNNLPCIVDFGLTRLRLVNLVSYNVLEW  
FLATGGEAAFELETDLDSHNQLLFFPLLPQYSKLRTLTLLRDNNMGFYRDLYNTSSPREMV  
AQFLLVDGNVTNITTVSLWEEFSSSDLAFLDMSQNFQYLPDGFRLKMPSLSHLNLH  
QNCLMTLHIREHEPPGALTELDLSHNQLSELHLAPGLASCLGSLRLFNLSNQLLGVP  
LFANARNITTLDMSHNQISLCPLPAASDRVGPSCVDFRNMA SLRSLSLEGCGALPDC  
PFQGTSLTYLDLSSNWGVNLGSLAPLQDVAPMLQVLSLRNMGLHSSFMALDFSGFGNLRD  
LDLSGNCLTTFFPRFGGSLALETDLRRNSLTALPQKAVSEQLSRGLRTIYLSQNPYDCCG  
VDGWGALQHGQTVADWAMVTCNLSSKIIRVTELPGGVPRDCKWERLDLGLLYLVLIIPSC  
LTLVACTVIVLTFKKPLLQVIKSRCHWSSV

**Important features of the protein:****Signal peptide:**

Amino acids 1-18

**Transmembrane domain:**

Amino acids 651-672

**N-glycosylation sites:**Amino acids 21-25;74-78;155-159;232-236;292-296;309-313;  
312-316;408-414;427-431;500-504;622-626**Glycosaminoglycan attachment site:**

Amino acids 533-537

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 566-570

**N-myristoylation sites:**Amino acids 24-30;39-45;45-51;141-147;199-205;245-251;  
308-314;396-402;416-422;420-426;471-477;  
484-490;497-503;522-528;545-551;555-561;610-616**Prokaryotic membrane lipoprotein lipid attachment site:**

Amino acids 657-668

**Leucine zipper patterns:**

Amino acids 48-70;492-514

566/615

**FIGURE 561**

TGGCCTACTGGAAAAAAAAAAAAAAAAAAAAAAAAAGTCACCCGGGCCCCGCGGTGGCCACAACAT  
GGCTGCGGCGCCGGGGCTGCTCTTCTGGCTGTTTCGTGCTGGGGGCGCTCTGGTGGGTCCCGGG  
CCAGTCGGATCTCAGCCACGGACGGCGTTTCTCGGACCTCAAAGTGTGCGGGGACGAAGAGTG  
CAGCATGTTAATGTACCGTGGGAAAGCTCTTGAAGACTTCACGGGCCCTGATTGTCGTTTTGT  
GAATTTTAAAAAAGGTGACGATGTATATGTCTACTACAACTGGCAGGGGGATCCCTTGAAGT  
TTGGGCTGGAAGTGTTGAACACAGTTTTGGATATTTTCCAAAAGATTTGATCAAGGTACTTCA  
TAAATACACGGAAGAAGAGCTACATATTCCAGCAGATGAGACAGACTTTGTCTGCTTTGAAGG  
AGGAAGAGATGATTTTAAATAGTTATAATGTAGAAGAGCTTTTAGGATCTTTGGAAGTGGAGGA  
CTCTGTACCTGAAGAGTCGAAGAAAGCTGAAGAAGTTTCTCAGCACAGAGAGAAATCTCCTGA  
GGAGTCTCGGGGCGTGAACTTGACCCTGTGCCTGAGCCCGAGGCATTCAGAGCTGATTCAGA  
GGATGGAGAAGGTGCTTTCTCAGAGAGCACCGAGGGGCTGCAGGGACAGCCCTCAGCTCAGGA  
GAGCCACCCTCACACCAGCGGTCCTGCGGCTAACGCTCAGGGAGTGCAGTCTTCGTTGGACAC  
TTTTGAAGAAATTCTGCACGATAAATTGAAAGTGCCGGGAAGCGAAAGCAGAACTGGCAATAG  
TTCTCCTGCCTCGGTGGAGCGGGAGAAGACAGATGCTTACAAAGTCCTGAAAACAGAAATGAG  
TCAGAGAGGAAGTGGACAGTGCCTTATTATTACAGCAAAGGATTTTCGTTGGCATCAAATCT  
AAGTTTGTTTTACAAAGATTGTTTTTAGTACTAAGCTGCCTTGGCAGTTTGCATTTTGGAGCC  
AAACAAAATATATTATTTTCCCTTCTAAGTAAAAAAAAAAAAAAAAAAAAA

567/615

**FIGURE 562**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA131639
><subunit 1 of 1, 303 aa, 1 stop
><MW: 33900, pI: 4.81, NX(S/T): 2
MAAAPGLLFWLFLVGLWVPGQSDLGRRFSDLKVCGDEECSSMLMYRGKALEDFTGPD
CRFVNFKKGDDVYVYYKLAGGSLELWAGSVEHSFGYFPKDLIKVLHKYTEEELHIPADET
DFVCFEGGRDDFNSYNVEELLGSLELEDSVPEESKKAEEVSQHREKSPEESRGRELDVPV
EPEAFRAEDSEGEAFSESTEGLOGQPSAQESHPTSGPAANAQGVQSSLDTFEEILHDK
LKVPGESERTGNSSPASVEREKTDAYKVLKTEMSQRGSGQCVIHYSKGFRWHQNLSLFYK
DCF
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-22

**N-glycosylation site:**

Amino acids 294-298

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 30-34

**Tyrosine kinase phosphorylation site:**

Amino acids 67-76

**N-myristoylation sites:**

Amino acids 205-211;225-231;277-283

**Amidation site:**

Amino acids 28-32

568/615

**FIGURE 563**

GCCAGCCGTGGGATTAGGCTTCGCCGGCTACGATTGCGGCCCCCATCTTCTGACTTTTCCTCG  
TGTGACCCATCTTTTCAAATTCCTTACCTGAGGAAGGAGCCCGATTACAAGGATATTTACCT  
GCTCCTACCTGATCTAGGGACGAGGATGGGAAGACCGCCTGTGGCCATGAGCCCTCCCCGGT  
GCTCCTGGGGCTAAGGCTGGGGCTGCAGCCATGGGGCTGGGTCAGCCCCAGGCCTGGTTGCTG  
GGTCTGCCCACAGCTGTGGTCTATGGCTCCCTGGCTCTCTTCACCACCATCCTGCACAATGTC  
TTCCTGCTCTACTATGTGGACACCTTTGTCTCAGTGTACAAGATCAACAAAATGGCCTTCTGG  
GTCGGAGAGACAGTGTTTCTCCTCTGGAACAGCCTCAATGACCCTCTCTTCGGTTGGCTCAGT  
GACCGGCAGTTCCTCAGCTCCAGCCCCGCCTGTGTGGAGAGGAGCTGCTTGTGGGCAGTGAG  
GAGGCGGACAGCATCACCTTGGGCCGGTATCTCCGGCAGCTGGCACGCCATCGGAACCTCCTG  
TGGTTCGTGAGCATGGACCTGGTGCAGGTGCAGTGGCTCACGCCTGTAATCCAGCACTTCGG  
GACGCCAAGGTGGAAAGACCGCTTGAGCCCAGGAGTTCGAGGCTGCAATTGAGTATGATTGCA  
CCACTGCACTCCAGCCTGGGCGGCAGAGAAAGGCTCCATCTCTAAAAAAGAAGAGCTAAGTG  
CTGTACCTAAAACATGCAGTATATAAACTGGCTGAACTTAGAAATAAACTGTTTTCATGTTAT  
GAAAA

569/615

**FIGURE 564**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA131649
><subunit 1 of 1, 153 aa, 1 stop
><MW: 17603, pI: 7.42, NX(S/T): 0
MGLGQPQAWLLGLPTAVVYGSLALFTTILHNVFLLYYVDTFVSVYKINKMAFWVGETVFL
LWNSLNDPLFGWLSDRQFLSSQPRLCGEELLVGSEEADSITLGRYLRQLARHRNFLWFVS
MDLVQVQWLTPVIPALRDAKVERPLEPRSSRLQ
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-20

**N-myristoylation sites:**

Amino acids 4-10;12-18;93-99

**Leucine zipper pattern:**

Amino acids 102-124



570/615

**FIGURE 565**

CGGCACGAGTAAAATGGAGATAATATCACCAATGCACTCAGCCCTAGCCACTGCATTGCTGTTA  
CTGATACCATTACTGCTGCTACGTCGTTTTTTTGGATGGCTCAGCCCTTAGGGAAGGGGGATCA  
AGGGAGAAGCCCGGACCTTCCCGCAGGAGGTGGGCTGGGCACAGCCCTGAACCATGGAGGTCA  
CCCACCCTGAGGTGCGGGACCTGGGTTCCTTCCTATCCACTGGGGGTCCCAGCCTTTGTCTTC  
ATCTCTCCAGGTCCCAGCCCTTCACAGTGGGCACTTCCTGCCTGTGACGGAGGCCCCAGCCA  
TCTCC

571/615

**FIGURE 566**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA131652
><subunit 1 of 1, 89 aa, 1 stop
><MW: 9688, pI: 11.49, NX(S/T): 0
MHSALATALLLLIPLLLLRFFDGSALREGGSREKPGPSRRRWAGHSPEPWSPTLRSGP
GFPSYPLGVPAFVFISPGSPSQWALPCL
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-18

**Glycosaminoglycan attachment site:**

Amino acids 58-62

572/615

**FIGURE 567**

AGTCTAGCAGGAAAGGAGAGGGAGCTTTCCCCGAAGACCCTCCTGGACCAGCCCCAGGCTCCT  
GTGCTGGTTGCACGCCAGGGCCTGTACTGACCACCTCCACGTGCCACTGGGGCTGTAAGGAGGA  
**ATGGCGGCCGTGGGCAGCCTGCTTGGCCTGGCAGCCTCTTCCTGGCTAGGGGGCCAGAACGCC**  
TCTGACCACAGCCTGTGGCTCCTGAGGAAGCCCCGAGGCTCATCCTGCCCCGGCACGGGTCAC  
CAGCTCTGCCGGCTGAGGCAGAGCACCGTGAAGGCCACCGGACCTGCACTCCGCCGCCTGCAC  
ACATCCTCCTGGCGAGCTGACAGCAGCAGGGCCTCACTCACTCGTGTGCACCGCCAGGCTTAT  
GCACGACTCTACCCCGTGCTGCTGGTGAAGCAGGATGGCTCCACCATCCACATCCGCTACAGG  
GAGCCACGGCGCATGCTGGCGATGCCCATAGATCTGGACACCCTGTCTCCTGAGGAGCGCCGG  
GCCAGGCTGCGGAAGCGTGAGGCTCAGCTCCAGTCGAGGAAGGAGTACGAGCAGGAGCTCAGT  
GATGACTTGCAATGTGGAGCGCTACCGACAGTTCTGGACCAGGACCAAGAAG**TGAC**CCGTGGCTC  
CAGCCACCCCGGGACATTGCTAAGATGGGAGGGCTGTTCTTAAATCACTCGTTCTTGAAGCTGC

573/615

**FIGURE 568**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA131658
><subunit 1 of 1, 164 aa, 1 stop
><MW: 18903, pI: 11.08, NX(S/T): 1
MAAVGSLGLAASSWLGGQNASDHSLWLLRKPRGSSCPGTGHQLCRLRQSTVKATGPALR
RLHTSSWRADSSRASLTRVHRQAYARLYPVLLVKQDGSTIHIRYREPRRMLAMPIDLDTL
SPEERRARLRKREAQLQSRKEYEQELSDDLHVERYRQFWTRTKK
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-18

**N-glycosylation site:**

Amino acids 20-24

**N-myristoylation sites:**

Amino acids 5-11;9-15;17-23;18-24

574/615

**FIGURE 569**

GGTGCCAAGGGTTTCGGGGGGGAGCACTGAGGCTTTAGCAGCTCTCCTGTATCCTCATTGTCAT  
CCTCCTGTAGCAGCTGGAAAATTCAGATTACAGGTGAAATTCCTGGCTGGCAATCTTCTGTA  
TATGGACACAGTGATGTGCCAGAAGGGCTTTGCATCCCTGAGACTGAAGGAAGCTCCATTTTT  
GGAGCCCTCCACACCTTGCTCTGTGTGCCTCTCATTCTGATTTGAATTCCTATTTTTGCTATA  
TGATGAAGCTGTAATCCTAAGTTTAAAAAGGGGAGTAGGTATTGACATCATGGTAGAAATAGG  
CTGTCTTATGGAAGTGTAGTTAGGGATCACAGCCTATTGGACCAGCCCCAGCCTTAGCAGCAG  
TTCTGTACACTGATTCTTCCAGATTAGTCTACGTTCCCTCGAACAGACCTATGCCATGGGTTA  
CAACTACAATTTGTTGTCGATTAGAGTTAACTTACAGACTCTCAAAACCCCATTTCTTTGGGTT  
TAGGCAACTTCCAGAAGTAGTCATTTATTTGAATTTTAGTCTAAGATCAACTGAATTAGGGAG  
GTTTGAAAGTGTAAGCAATCGTACATTCCCAAACACTTTGTAAAGAAGGAATGGGTAGTG  
TCAACTAAAGGAAATGGTGTGCATCCCAGCAAAAGAAAGAGACCGAAAGCAAAGTCATAAACC  
**ATG**CCCCACGAGCTCAGCTGTCCTGCTCCGTGTCTCTCCATAACCCTTGTTGACTGTGCTCATA  
TTAGCCAGAGACCTAAGTGTCTTTGGAGGATGTCCCTGGGGCCCCCTCCCCCTCCGCTGTCAC  
TGTCTACTTCCTGATCCTCTCTTCTGTGCAGGAGAGGTCCAGGCCTTCTATGAGGACCTGAGT  
GGCCGGCAGTACGTGAATGAAGTCTTCAACTTCAGCGTGGACAAGCTCTATGACCTCCTCTTC  
ACCAACTCGCCCTTCCAGCGGGATTTTCATGGAGCAGCGGCGCTTCTCTGATATCATCTTCCAT  
CCATGGAAAAAGGAGGAGAATGGAAACCAGAGCCGAGTGATTCTTTACACCATCACCTTACC  
AACCCTCTGGCTCCCAAACACTGCCACTGTCAGGGAGACACAGACCATGTACAAGGCGAGCCAG  
GAGAGTGAATGTTACGTGATAGATGCCGAAGTCTCACCCACGACGTGCCCTACCACGACTAC  
TTCTACACAATCAATCGCTACACGCTCACCCGTGTGGCTCGGAACAAGAGCCGACTCAGGGTC  
TCCACAGAGCTGCGCTATCGAAAACAGCCCTGGGGGTTAGTGAAAACGTTTCATCGAGAAGAAC  
TTCTGGAGTGGGCTGGAGGACTACTTCCGCCATTTAGAGAGCGAGCTGGCCAAAACGGAGAGC  
ACTTATTTGGCTGAGATGCACAGACAATCTCCCAAAGAGAAGGCCAGCAAGACTACAACGGTG  
CGGAGGAGGAAGCGTCCCCATGCCACCTGCGAGTCCCTCACCTGGAAGAGGTGATGAGCCCCG  
GTCACCACGCCCACAGATGAGGATGTGGGCCACAGGATCAAACATGTGGCAGGTTCACACAG  
ACGCGGCATATCCCGGAGGACACCCCCAACGGTTTCCACCTGCAGAGCGTGTCCAAGCTGCTG  
CTGGTTATCAGCTGTGTTCTGGTGCTGCTGGTCATCCTTAACATGATGCTCTTCTACAACTC  
TGGATGTTGGAATACACCACGCAGACCCTCACTGCCTGGCAGGGTCTAAGGCTCCAAGAAAGG  
TTACCCAGTCTCAGACAGAATGGGCCCAGCTCTTAGAGTCCCAACAAAAGTACCACGATACT  
GAGCTCCAAAATGGAGGGAAATCATCAAATCCTCAGTGATGCTCCTTGACCAGATGAAGGAC  
TCGCTCATCAACCTTCAGAACGGCATCAGGTCCCGCGACTACACGTCGGAAAGTGAAGAAAAG  
AGGAATCGCTATCAT**TGA**CAAGGCAGGAACAGGGTGGCTGCAAGAGGCCTGTGCAATACATGT  
ACATAGACCATATAAATATATATATATAAATATATATATATACAGAATATAAATATATATATT  
ATATACAGATTTTAAAAAAGAGATAATGCCTATGTACCAGGGAGAAGGAGCGGGCCCTCCCGC  
GCCCTGTGCTGGCCGGAGCAGCGTTTTCTTATGGTGGAGCAGCTGAGGAGGGCAGGAACCGCC  
TCTCAGCACCGACCTCCCCTGATCTCCCTCCTCCACCCCTCTGTTCCCCACCCCTTCCCTTGC  
TGGCCATTCTTGGCTTTTAGAAGGGAAATGTTGAGCCAAAGTTATGCCTGCGAAGACCCTAAG  
GTCTCAAAAAGAAGTCTTAAGACGGCATTGCTTAAGGTGCTTCATTCCCTAATCCCCTTTTGA  
TTTGTTTCCAAAATAAAAGAGAATCTTTCTTCCCTAAAAA

575/615

**FIGURE 570**

><subunit 1 of 1, 425 aa, 1 stop  
><MW: 49786, pI: 8.84, NX(S/T): 3  
MPTSSAVLLRVLSIPLLTVLILARDLSALGGCPWGPLPLRCHCLLPDPLFCAGEVQAFYE  
DLSGRQYVNEVFNFSDKLYDLLFTNSPFQRFMEQRRFSDIIFHPWKKEENGNSRVIL  
YTITLTNPLAPKTATVRETQTMYSQSECECYVIDAEVLTHDVPYHDYFYTINRYTLTRV  
ARNKSRLRVSTELRYRKQPWGLVKTFIEKNFWSGLEDYFRHLESELAKTESTYLAEMHRQ  
SPKEKASKTTTVRRRKRPAAHLRVPHLEEVMSPVTTPTDEDVGHRIKHVAGSTQTRHIPE  
DTPNGFHLQSVSKLLLVISCVLVLLVILNMMLFYKLWMLEYTTQTLTAWQGLRLQERLPQ  
SQTEWAQLLESQQKYHDTLQKWREIIKSSVMLLDQMKDSLINLQNGIRSRDYTSESEEK  
RNRYH

**Important features of the protein:****Signal peptide:**

Amino acids 1-28

**Transmembrane domain:**

Amino acids 312-334

**N-glycosylation sites:**

Amino acids 73-77;114-118;183-187

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 97-101

**Tyrosine kinase phosphorylation sites:**

Amino acids 144-153;188-196

**N-myristoylation sites:**

Amino acids 201-207;291-297

**Leucine zipper pattern:**

325-347

576/615

**FIGURE 571**

GTAGAGAGTGAAGCAGCAAGACTGCAGAGCCTCATCAAGAAGTGTGGAGTGAAGGGAAGGCTTCAGATGGACAAT  
TTGTGTGCTGGGGAAAAAATGGAATGTGCTGCAAATTTCCCCTGTGGATAAGGGTGGACGGCTGCTCTGTCAACTT  
TGACCATTTTCAGATTCTGCGGGCCATTGGTAAAGGGAGTTTTGGAAAGGTATGCATCGTGCAGAAGCGAGACAC  
TAAGAAAATGTATGCAATGAAGTACATGAACAAGCAGAAGTGCATCGAGAGGGATGAGGTTCCGAATGTTTTCCG  
GGAGCTGCAGATCATGCAAGGGCTGGAGCACCCCTTCTGGTCAATCTGTGGTACTCCTTCAGGATGAGGAGGA  
CATGTTTCATGGTGGTGGACCTGCTCCTGGGAGGCGACCTGCGCTACCATCTGCAGCAGAATGTGCATTTACAGA  
GGGACTGTGAACTCTACATCTGTGAGCTGGCACTGGCCCTGGAGTATCTTCAGAGGTACCACATCATCCACAG  
AGACATCAAGCCAGACAATATCCTGCTGGATGAACACGGACATGTTACATTACAGACTTCAACATAGCGACGGT  
AGTGAAAGGAGCAGAAAGGGCTTCCCTCCATGGCTGGCACCAAGCCCTACATGGCTCCAGAAGTATTCCAGGTGTA  
CATGGACAGAGGCCCCGGATACTCGTACCCTGTGCACTGGTGGTCCCTGGGCATCACAGCCTATGAGCTGCTGCG  
GGCTGGAGGCCGTACGAAATCCACTCGGTACGCCCATCGATGAAATCCTTAACATGTTCAAGGTGGAGCGTGT  
CCACTACTCCTCCACGTGGTGCAAGGGGATGGTGGCCCTGCTGAGGAAGCTCCTGACCAAGGATCCTGAGAGCCG  
CGTGTCCAGCCTTCATGACATACAGAGCGTGCCCTACTTGGCCGACATGAACTGGGACGCGGTGTTCAAGAAGGC  
ACTGATGCCCCGCTTGTGCCAATAAAGGGAGGTTGAACTGCGATCCCACATTTGAGCTTGAAGAGATGATTCT  
AGAATCCAAGCCACTTCACAAAAAGAAGAAGCGATTGGCAAAGAACAGATCCAGGGATGGCACAAAGGACAGCTG  
CCGCTGAATGGACACCTGCAGCACTGTTTGGAGACTGTCCGGGAGGAATTCATCATATTTCAACAGAGAGAAGCT  
CAGGAGGCAGAGGGACAGGGCAGCCAGCTCTTGGACACCCGACAGCCGAGGGGGAGGCCAGGCCCAAGCAAGCT  
CCAGGACGGGTGCAACAACAACCTCCTCACCCACACCTGCACCCGTGGCTGCAGCAGCTGAGGCCACACTTGTG  
CTGCTCAACAGGACTGCACTCGTCTCTGCCCTGCCACCCAGAGCCCCTCTTTGTGCCCTGATGGTCCCTGTCTC  
ACCCCTGAAAACATCAGATGCAGAAAAAGCCCTGGACTTGGAGCTGGGAAGCCTGGGTTCTGGTCCCATCTCCAT  
GACTGATTCACGTGTGACCTCAGACAAGTCACGCCCTCTCTGTGCCCTCCGTTTTCTGCATCTGCCAAAGGGGTTA  
AACACTTCTGCCCCACTTCAAATTACAAGATTATGGGAGAAACCAATTAGGTAGGAAACATGAAAAACCTTTGA  
TATTTATAAAATCATTTTTTACGTGCAAAATATAACCTTAATATTTGAAGTGACCCCATTTCCCAAAGCAATCAA  
ACCGTCATGACTTTGCAATTTGGCACATCCTAGCTTGTAGAGGGCACTTCCGAAAAACAGCCCTGACAGCAA  
AATAAAGGTCTGATATGTTGGCCCCCTTCTATGGAAACAACGCTGCCAAATCCTGGAGCAAAACCTGAAGTGTCTT  
CATGTGCATTTCTCTGGCAGGCCACAGTCCTTCTGAGCTTGTAAAGATGGTGCAGCATGCAGACCAGACTTGTCCCC  
AAGGTCTCAGCGCTGCGGTCTCACTCCTCCCTCATTTAAGAAGACTATCCTTACCTTTTAGTTTCAGCAGTCCT  
CACCACCACCATATCCCCAGTGCTGGGATGGCACACAGGTGTCCATTGAGATGAGAGTTGGGTGCTGAGCATTG  
GTTACTCCTGCAGAGTGTAATCAGCACCCCATCCAAGTGGCCCCGAAAGCCCAGACCTGCAGCAGAACTCTCCAAC  
TCTCTATCAGCTTTCAGGGTTTTCTCTCCTGGGAAGGGTGTAAATCAGCTTGTGAGATTCTTCTTACAGAGAGT  
ATCCAATCGGTATTGGTGGAGCGGCTCCCTATTTATACAATAGGAAGCATGGGTGCTTAGAAAGTTTATTTTCAGG  
AGGAAAATGGGTTACACAAAAAGCAAACCTACATTTCTGATCTGCTCAGGGAGAAGCTTGCCTTTGAACTGGAAGA  
TGTTGGGATGAGCAGGGAAAGCTTAGACTTTGGAGTCAGGTTTGTGTTGAGAATCCAGCCCTGCTGGCTACTAAC  
TAACTGGGAGACCTTAGGCAAAGCATGCAATCGCTCTGAATGGCAGTTTCTCATTTTTTAAACAGGGATAATAAA  
ACTAATATTGAGGGGAGTTACAGGGTTAAATAAGATCCTGTGTGTAACCCCAAGCATTGGATGACTCATAGAAT  
GGCCTTTTTTGTGAGCATAATCGTCATCATTTATTTAGATACTTTCTTCTTCACTCACCCAGCAGGTGAGTTTTC  
TGTGCAACAAACCTGTTTAGGATTCTTCCAAATGTTCTTCTGGGGTCTTTGATATTTGTTTGTACATCCTGCG  
TGAAGTTCGACTGTGTTTTTATTTTTTTCATCCAACCTCCATTTTTTCACTTTTTTACATGATTACTCAATCCTTGGG  
GCTGTCCATGTGATCTCTTAGATTTCTTAAAGACATTTTAATGTATGGTTAGGTTTTATTTTTTATTTTTTAA  
AAAAGAAATAGTCAGTGTTCCTCCTTTCAACCGAGACTATTTCTGGATTGTGTGCTCCTCGTCAGTTGACTTGT  
TTTGACACTTTTTCTTACTTCATGTCCCATCAACAACCGTCTGCTCCCCACCTCCCCAGGAAATAAGGGGC  
CTGCTCCTCTCCCTACTGTGACCCTGGAGGCTCTTAAGATGATGATGGTTTTTTTTTATTTGGGCTGAGTTCACGAA  
TTAGGGGCAGGAGCTGGAAGTCGCCCTAGGAACACCAGATTTCTGGTCTGTTCAAGTTGGCATTCTTGTGTTG  
GAATAAACTATTTCTTGG

577/615

**FIGURE 572**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA136110  
<subunit 1 of 1, 364 aa, 1 stop  
<MW: 42195, pI: 7.40, NX(S/T): 1  
MKYMNKQKCIERDEVNRNVFRELQIMQGLEHPFLVNLWYSFQDEEDMFMVVDLLLGGDLRY  
HLQQNVHFTEGTVKLYICELALALEYLQRYHIIHRDIKPDNILLDEHGHVHITDFNIATV  
VKGAERASSMAGTKPYMAPEVFQVYMDRGPYSPVDWWSLGITAYELLRGWRPYEIHVS  
TPIDEILNMFKVERVHYSSTWCKGMVALLRKLLTKDPESRVSSLHDIQSVPYLADMNWDA  
VFKKALMPGFVPNKGRLNCDPTFELEEMILES KPLHKKKKRLAKNRSRDGTDKSCPLNGH  
LQHCLETVREEFII FNREKLRRQQGQGSLLDTSRGGGQAQSKLQDGCNNNLLTHTCTR  
GCSS

**Important features of the protein:****N-glycosylation site:**

Amino acids 285-289

**N-myristoylation sites:**

Amino acids 123-129;290-296;337-343;339-345;348-354

**Serine/Threonine protein kinases active-site signature:**

Amino acids 92-105



**FIGURE 573**

CTCCAGTTTCGCCGACTGTAACATGTTTCATCCAGTTCAGTATGTTTTGTATGCAAGTTGGAATAATAAATAAACGCTC  
CTGAACTGGATGAAACATGTTACAGTCGGCCGAAACATGAGAGGCTGTGTGAGAAGCTGCAGCCGCCGGCAGAGG  
AGACCTCAGCATCATCTAGAGCCAGCGCTGGCCCTGCCTCCGCCTGCGCCGCCGCCCGCTCGCCGTTTCTGTT  
CCTGCTACTGTCCCACCTAAACAACCTCCCGTTACACGGACAAGTGAACATCTGTGGCTGTCTCTCTCTTTCTTC  
CTCTCTTCTCAACTCCTTCTCTCTCTCCACTTCCCAGCCGACGAGAAGCCCCAACCCAACTGACGCTGGCA  
CAACTGCAACCGGTTCATCCGCACAACCTTATCTCGTCTCTCGGCTCCCCTAAGGCATTGGACCCATCGCCG  
GTCTTTTATTTTGCAAAGTTGCATCGTGTACATATTTTGTCCCCGCCACCTCCCTCTGTCTCTGGAGTCCCT  
TACAGCCCCGCAAACTCCTCCTGGAGCTGCGCCCTAGTGCCCTGCTGGGCAGTGGCGTTCCCCCCCATCCTCCC  
GCGCCAGCCCTGCTGCTCTGGGCAGACGATGCTGAAGATGCTCTCCTTTAAGCTGCTGCTGCTGGCCGTGGCT  
CTGGGCTTCTTTGAAGGAGATGCTAAGTTTGGGGAAAGAAACGAAGGGAGCCGAGCAAGGAGGAGAAGGTGCCTG  
AATGGGAACCCCCGAAGCGCTGAAAAGGAGAGACAGGAGGATGATGCTCCAGCTGGAGCTGCTGAGTGGGGGA  
GAGATGCTGTGGGTGGCTTCTACCTCGGCTGCTGCTGCTGCTGCGGAGTACAGCCCGGGGCTAGGGCGCTCT  
GAGAATAAGATATTTTCTGTTACCAACAACACAGAATGTGGGAAGTTACTGGAGGAAATCAAATGTGCATCTTTGC  
TCTCCACATTCTCAAAGCCTGTTCCACTCACCTGAGAGAGAAGTCTTGGAAAAGAGACCTAGTACTTCTCTGCTC  
TGCAAAGACTATTGCAAAGAATTCTTTTACACTTGCCGAGGCCATATTCCAGGTTTCTTCAAACAACCTGCGGAT  
GAGTTTTGCTTTTTACTATGCAAGAAAAGATGGTGGGTGTGCTTTCCAGATTTTCCAAGAAAACAACTCAGAGGA  
CCAGCATCTAACTACTTGGACAGATGGAAGAATATGACAAAGTGAAGAGATCAGCAGAAGACAAACAACAAC  
TGCTTCTGTATTACAGGAGTTGTGAGTGGGCTGCGGCACCGGTTGGTGCCCTGCATAGTGGGGATGGCTCGCAA  
CGTCTCTTCATTCTGGA AAAAGAGGTTATGTGAAGATACTTACCCCTGAAGGAGAAATTTTCAAGGAGCCTTAT  
TTGGACATTCAAAACTTGTTCAAAGTGAATAAAGGGAGGAGATGAAAGAGGACTGCTAAGCCTCGCATTCCAT  
CCCAATTACAAGAAAAATGGAAGTTGTATGTGTCTATACCAACCAAGAACGGTGGGCTATCGGGCCTCAT  
GACCAATTCTTAGGGTTGTGGAATACACAGTATCCAGAAAAATCCACACCAAGTTGATTTGAGAACACGCCACA  
TCTTTTCTTGAAGTTGCAGAACTCCACAGAAAGCATCTGGGAGGACAAGTCTTTTGGCCCTGACGGCTTTTGT  
TACATCATTTCTTGGTGATGGGATGATTACACTGGATGATATGGAAGAAATGGATGGGTAAAGTATTTACAGGC  
TCAGTGCTACGGCTGGATGTGGACACAGACATGTGCAACGTGCCTTATTCATACCAAGGAGCAACCCACACTTC  
AACAGCACCAACCAGCCCCCGAAGTGTGCTCATGGGTCCACGATCCAGGCAGATGTGCTGTGGATAGACAT  
CCCATGATATAAAACATCAATTTAACGATACTGTGTTCAGACTCCAATTGAAAAAACAGATTCACGCCAGAATT  
CTACAGATAATAAAGGGGAAGATTGAAGAGTGAGCCATCACTTTTGAAGTTCAAGCCATTAGTAATGGTCCT  
TTGGTTGGTGATTTGTATACCGGGCTGCCAGTCAAGAAAGATTGTATGGAAGCTACGTGTTTGGAGATCGTAAT  
GGGAATTTCTAACTCTCCAGCAAAGTCTGTGTGACAAAGCAGTGGCAAGAAAAACCCTCTGTCTCGGCACTAGT  
GGGTCTGTAGAGGCTACTTTTCCGGTCACATCTTGGGATTGTGGAGAAGATGAACTAGGTGAAGTTTACATTTTA  
TCAAGCAGTAAAAGTATGACCCAGACTCACAATGGA AAACCTTACAAAATTGTAGATCCCAAAAGACCTTTAATG  
CCTGAGGAATGCAGAGCAACGGTACAACCTGCACAGACACTGACTTCAGAGTGCTCCAGGCTCTGTGCAAAACGGC  
TACTGCACCCCAACGGGAAGTGTCTGCTGAGTCCAGGCTGGGAGGGGACTCTGCAGAGACTGCAAAATGTGAG  
CCAGCATGTGCTCATGGAGGTGTCTGTGTTAGACCGAACAAGTGCCTCTGTAAAAAAGGATATCTTGGTCCTCAA  
TGTGAACAAGTGGACAGAAACATCCGCAGAGTGACCAAGGCAGGTATTCTTGATCAGATCATTTGACATGACATCT  
TACTTGCTGGATCTAACAGTTACATTGTATAGTTTTCTGGGACTGTTTGAATATTCTATTCCAATGGGCATTTAT  
TTTTTATCCTGTCATTA AAAAAAAAAAAGACTGTTATCCTGCTACACACTCCTGTGATTTTCATTCTCTTTTATTAA  
TTTAAAAATTAATTTCCAGAAATGTGCAGATCCTCTGTGTGATGTGATGTCAGCATGTTTGGTTCACATATGCACATAC  
ATACTATAAACCCTATATGCGTGTGTGCATAACAGATGATTTTTTAAATATAATACTTCTATGCAAAAGTAAAT  
TTACACAGAAATTCCATTGTAAATTGATAATGATTTTTTATGTTACTAGAAGAGATTATTTTGCATTCCCAGGAA  
TTTTCTGTCTGTAATCACTAAAGTCAACTTTAATAGAGTTTTTGAACAGTACTGTGCAATCCGATGGATCTAATT  
AAAAAAAAGGCAATATTTTTATATTAAGTACTATACTAGGAGAGAATGTTTCAGAACTCCCTGATGAATTTCTA  
AGTGAGCAACTTGATATAAAATTTGAATCTTCATTTTTTGTGAGTGTATCCAGTTACAGAATGTACACACTTACC  
TTTTTATGGCTGAGAAATCTGTTTATTTTATCTTAATCTCAAGATTGTTTTCAAGTGTTTTATAATTAAATCAT  
AATAGCATGTTTTTAAATCAAAAA

579/615

**FIGURE 574**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA139592  
><subunit 1 of 1, 882 aa, 1 stop  
><MW: 98428, pI: 8.89, NX(S/T): 5  
MKHVTVGRNMRCVRSRQRRPQHHLPSAGPASACAAA AVSVPATVPPKQLPLHG  
QVNICGCPLLFLLFQLLLLLPLPSRSRKPPQTQLTALQLQTVSSAQLYLAPRAPLRHWTH  
RRVFFYCKVASLYIFLSPPPPSVSGVPYSPANSSWSCALVPLLGSVPPHPPAPSPCCSG  
QTMLKMLSFKLLLLAVALGFFEGDAKFGERNEGSGARRRRCLNGNPPKRLKRRDRRMMSQ  
LELLSGGEMLCGGFYPRLSCLLSDSPGLGRLENKIFSVTNNTTECGKLLLEEIKCALCSPH  
SQSLFHSPEREVLERDLVLP LLCKDYCKEFFYTCRGHIPGFLQTTADEFCFYARKDGG  
CFPDFPRKQVRGPASNYLDQMEEDYKVEEISRKHKHNCFCIQEVVSGLRQPVGALHSGDG  
SQRLFILEKEGYVKILTPEGEIFKEPYLDIHKLVQSGIKGGDERGLLSLAFHPNYKKNK  
LYVSYTTNQERWAIGPHDHILRVVEYTVSRKNPHQVDLRTARVFLEVAELHRKHLGGQLL  
FGPDGFLYIILGDGMITLDDMEEMDGLSDFTGSVLRDLVD TDMCNVPYSIPRSNPHFNST  
NQPPEVFAHGLHDPGRCAVDRHPTDININLTILCSDSNGKNRSSARILQIIKGKDYESE  
SLLEFKPFSGNGLVGGFVYRGCSERLYGSYVFGDRNGNFLTLOQSPVTKQWQEKPLCLG  
TSGSCRGYFSGHILGFGEDELGEVYILSSSKSMTQTHNGKLYKIVDPKRPLMPEECRATV  
QPAQTLTSECSRLCRNGYCTPTGKCCCSPGWEGDFC RTAKCEPACRHGGVCVRPNKCLCK  
KGYLG PQCEQVDRNIRRVTRAGILDQIIDMTSYLLDLTSYIV

**Important features of the protein:****Transmembrane domains:**

Amino acids 63-80;186-201

**N-glycosylation sites:**

Amino acids 152-156;281-285;598-602;629-633;641-645

**Glycosaminoglycan attachment site:**

Amino acids 417-421

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 856-860

**N-myristoylation sites:**

Amino acids 12-18;413-419;457-463;698-695;720-726;723-729

**EGF-like domain cysteine pattern signatures:**

Amino acids 805-817;837-849

580/615

**FIGURE 575**

CGGCTCGAGAGCGGGGCAAACCTGCTTGGCACCTCTTCAATAGGTGACATTCAATGATAGATCT  
CTGGCTTCCTGCTCTGTTTGTCTGGTTGCCCTGGAAAGCCTGCTGCTCAGCCCATGCCCCGG  
GACTTCCTCCACCCTCACCAGGACATTCTTTCCATCTCTTGTCTCCTGTGTGCAAGTCCCTTT  
CTCCTGGATTCCATGTCTTGAATGTTTCTTAATTTACTTCCTCATTTTGGCAGAGGATGTCTT  
CCAGTTGTTTTCTGGGAATGCTAATATGCAAGTGAACCACTGACCTGCAGTTCTGCCCACACA  
GGGTTAATAACCAATCAGATTCTCTCTTTTCAAGATGGTTAACATAACAGACACCAAGAAAGG  
GAAGAGGAGCCGACAGCAGAGGGGGGAAGCTGAAAAGACGCACAAAGAATGGCCATAAAAGATA  
TGAGCAACCCCAGCTTTCCAGACAGTCACTTTTCCCAGTGGTCATACCTGGTCTGGAAGATT  
CCCATCATCTCGAATAAAGCTGTTGTTGCTTTTAACTCCATGGAGAGACCGAATGGAGTGAGC  
CCAGCAGGGCATGCTGGGCAAGAGAGGTCCCCGAGTCCCAAATAAGAATTTCAACTAGTATA  
AAACGAGGCAGCGAACCCACACGTGGAAGTCTGATACCGCTTGACAGAAGGGAATTGAATAGAT  
GTCTCCCTATTGGTAAGGATGTGGTTTTATTGACTTGAAATAACAAAGCCGCAAGCAACAAC  
TGATCATCCGCGGGATGCTGCCACAAGGAATAATTGAGCACTCATTGACAGACAGGGGAAACC  
ACTGCCTCTTTTCACTCTTTCTCCAGATTCCAACAGTCAGTGTTACAGCATTACCTTGTCTT  
ACCTCCCTGAGAAGACGTTGCAGCTCACTCACCCAGTGGGCACTGGGAGCCTCTGCTTCAAGT  
GGGAGACAGATGCCCCCACATGCACATCTGGTGTATGAAGCAGATACTGGGGCTTCATAA  
ACACAGAAGGGGCAGGGAAGTAGCCCCAGGGCATAGTGTGGGGCCTCCTGACTAAAAGTAGCTT  
GCAAACCCCTGCCTATAACAGCCACTTCTGGCAGTCATTGTGCCACTTAGGAGCCCTCCTCA  
CCGCTCTTCCTTTAGTTTCTTCACTCTGTATAGACCCTGCCAGAGCAGCTCAGGGTGGAGCAG  
CTGCAGCCATGGGACCTGCTCCAGGCAAGGCCCTATGCTACACAGTCCCTGGGGGTGAGGATT  
CCAGAGGAGTCAATTCCCTACCCGCCCTTCCAGGGGATGGCCGAGATGAGCGTTCCACAGGG  
AAAGTGAAAGTTGCAAGGCTGTTGCGGAAACACCAGGGGTTCATTTAGGTCTTGCTGCTCAT  
CTCACAGAAAGCCAGTCACTGAGACAAGTATTGTGAGGGAAGAAGGCTTTATCCAGGTGCTAC  
AGACAGGGTGAACAAGAGATCAGTCTCAAATCCATCATCACTGACTAAAATTAGGGGTT  
TATATAGCAGGGAAGAAATGTAACATGTGGGAAAACAGGGATTAACGAGGGGCAAGGAAG  
AGGAGTTGGCCAACAGGCAGCAGGTGGTCACTGGGGAATCATGATGGGTGAGGGGTCTGGCT  
TCTCACTTTCCAGATGTGGGGATCTGGTAAATTTCACTTCTTGATAACCGTCTGGGAGGATTG  
CTGGCTGGTTTTCTGAGAAAGGAATTCAGATGACATAAATGTAAATTTCTCCTTGGGTTTCAA  
GACTGAGAGGGTCAATTTCTAGGTTTATTCAAGAAAACCATAAACATCAGTTCTATGGGACA  
ATTGGGCCCATTTCAAGGCTCTGAGGATAAGGGTTAATGAGGGGACAGAGTCGCCTGGAGAAG  
TTCACTGGGGCCTACAAGAACTAGAGAGGCTTCTGGCAAAGCTCTATGCTGTCTATCCTCT  
CTTCTCTCCTTGCAGGAAGATTCCAGTATAATAGACCCGAGGTGAAAAGGCTTTTGTTCATA  
AGTAGAAAACCTGAAGGGGGGTGGGAGGCACATGGATTTGAACCAGAGACCGCTTGGCCTGCAG  
GCAAATGCTGTACCTTCAGTTGCACCCCTCACTTGTTACAGCTGTTTCTGATAAGCACTTGTG  
CAGCCCCATCAGCACCTCGATTTCTTCTTGGTGAGTCCATGGGAACAGCCCCACTGCAAACAA  
CCCATTCTGCTCTCCTCTTTTCTTCTAAACCTCAACCTCCTCCTACCTGGCAGTCCACAGGCC  
TACAGCTTCTCCTCAGTGGGAAAGACATCAGCTTGGAAAACCACTTGGAAAGCCAACGTTATC  
CTAGAAAAGCTTTTTTAAATGACCCAGCAGGACAAGTCTCCGGATGGCCTTGGCCAACCCGGTG  
CTTCCCTCTTTTCTTGGTTGTAGTTCTCAGAATAACTAGAGAATGTACTGGGAGTGTTGTCTT  
GAGATAAGGAGGAACGTCTCTAAACCTGGACTCTGTTCCCATCACACCTAGAACAGGATGTCC  
TGCAACGCTTTAGCCCAATGATCCAAGTTGCCCTTGGGGTATAAACTTGACAGCAGAGGGCG  
TTCAGGGTCCCTCAGCTGCAGTGTGAAGTGGGACACACAGGTGAGACTCCATCTGCCCTGGGC  
AGGTTCTTGAGCCTTGGGGGACCAGTTTACCCTACATCCCAGGCTTCTGTTGTCCCTTGCCTG  
CCTGTAAGGAATAAAGTTGCTTTGCTTA

581/615

**FIGURE 576**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA139608  
><subunit 1 of 1, 80 aa, 1 stop  
><MW: 8927, pI: 3.77, NX(S/T): 0  
MIDLWLPALFVLVALESLLLSPCPGTSSTLTTRTFFPSLVSCVQVPFSWIPCLECFLIYFL  
ILAEDVLQLFSGNANMQVNQ

**Important features of the protein:****Signal peptide:**

Amino acids 1-29

**Transmembrane domain:**

Amino acids 47-62

**N-myristoylation sites:**

Amino acids 25-31

582/615

**FIGURE 577**

ATCGGTTAGCGCCTTGCCATGATTAATCCAGAGCTGCGGGATGGCAGAGCTGATGGCTTCATA  
CATCGGATAGTTCCCAAGTTGATACAAAAGTGAAGATTGGCCTTATGTGCTTCCTGAGTATT  
ATTATTACTACAGTTTGCATTATTATGATAGCCACATGGTCCAAGCATGCTAAACCTGTGGCA  
TGTTTCAGGGGACTGGCTTGGAGTGAGAGATAAGTGTCTATTTTCTGATGATACCAGAAAT  
TGGACAGCCAGTAAATATTTTGTAGTTTGCAGAAAGCAGAACTTGCTCAGATTGATACACAA  
GAAGACATGGAATTTTGAAGAGGTACGCAGGAAGTATGCACTGGATTGGACTAAGCAGG  
AAACAAGGAGATTCTTGGAATGGACAAATGGCACCACATTCAATGGTTGGCCATCAAACCTCC  
AAATGGTCTTGCAACTGGAGCCTCCGACAATGGCTTCTTCTGCTGGGACCCCTTAGATTAGGCC  
TCTGAGGGAGCTCTGACTGCCGTTTCCCCAAAACAATGTCCCCTGTCAGCAGGAAGCAGTTAA  
ATCAGTCTTCATCCTTATCCTTAATATAACGGCAGTTAGATGTACTTCTTTAGAGGGAGTAAA  
TTTATCAATTCAGAGCAATTCATCCTCCTTTCCATCTTTGATTACAGTTAATAGGCTATA  
AATTTTGATAATGTAGAATAAACTACAGAAAACCTTCTTG

583/615

**FIGURE 578**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA143292
><subunit 1 of 1, 160 aa, 1 stop
><MW: 18576, pI: 9.29, NX(S/T): 3
MINPELRDGRADGFIHRIVPKLIQNWKIGLMCFLSIIITTVCIIMIATWSKHAKPVACSG
DWLGVRDKCFYFSDDTRNWTASKIFCSLQKAELAQIDTQEDMEFLKRYAGTDMHWIGLSR
KQGDSWKWTNGTTFNGWPSNSKWSCNWSLRQWLLLLGPLR
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-42

**N-glycosylation sites:**

Amino acids 78-82;130-134;146-150

**N-myristoylation site:**

Amino acids 131-137

584/615

**FIGURE 579**

TGAAGGCCTGTGAGTGAGGAATGCCTCTCACCAGCTGTGCCTGAGCTGCAGCACTCCAGCCAC  
TGCTGTCTCCTTAGCTGCTCACATATGGATACTTTCACAGTTCAGGATTCCACTGCAATGAGC  
TGGTGGAGGAATAATTTCTGGATCATCTTAGCTGTGGCCATCATTGTTGTCTCTGTGGGCCTG  
GGCCTCATCCTGTACTGTGTCTGTAAGTGGCAGCTTAGACGAGGCAAGAAATGGGAAATTGCC  
AAGCCCCCTGAAACACAAGCAAGTAGATGAAGAAAAGATGTATGAGAATGTTCTTAATGAGTCG  
CCAGTTCAATTACCGCCTCTGCCACCGAGGAATTGGCCTTCTCTAGAAGACTCTTCCCCACAG  
GAAGCCCCAAGTCAGCCGCCCGCTACATACTCACTGGTAAATAAAGTTAAAAATAAGAAGACT  
GTTTCCATCCCAAGCTACATTGAGCCTGAAGATGACTATGACGATGTTGAAATCCCTGCAAAT  
ACTGAAAAAGCATCATTTTGAAACAGCCATTTCTTCTTTTTGGCAAACTGAAGAGGGTTTAC  
ACAACTTATTTTAAACAATCAAGAATGGTTGAACTTCAGTAGGTCTCTGGGCCCTGAAAGCC  
AGTGGTGATTTTATGAAGCTCTATAAGATAAAGCACTTCCCAAACCTTAGATGAAGACACCCC  
TGCGATCGGATGACTGCAGCCAGAGGAGACACATGGGTGCTCGGCTCTGAGGACTTAGAGGGG  
TCAGCCTTGTGCTGTTGAGGAACTTCCATGGGAAGGACCACGGGGCTCCATGGCTCCCACC  
TGTGGGAACTACTCATTTCTTGGCATTTCTTCCCCCTTCATTCCCTTTGGTTTGCATGGTTC  
TGAGTGATATTAAATCTCAGCATTTGGTTGTGCAAAAAAAAAA

585/615

**FIGURE 580**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA144844
><subunit 1 of 1, 145 aa, 1 stop
><MW: 16618, pI: 5.26, NX(S/T): 1
MDTFTVQDSTAMSWWRNFWIILAVAIIVSVGLGLILYCVCKWQLRRGKKWEIAKPLKH
KQVDEEKMYENVLNEPVLPLPPRNWPSLEDSSPQEAPSQPPATYSLVNKVKNKKTVS
IPSYIEPEDDYDDVEIPANTEKASF
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-35

**Tyrosine kinase phosphorylation site:**

Amino acids 61-70

**Amidation site:**

Amino acids 48-52



586/615

**FIGURE 581**

GGCCGCCTCCGCGGGGCTGTGGGAAGCTTGGGCTGTCCCAGGACCGTCAGTCTCCTCCTCTGA  
CCCTCCCTTTCCCTTGTGTGTAGGGCCGCGTCCCACCCCCACCTCGCCGGAGTCCGGGGCG  
GCCCCGGTGTCCCTCCGAGCCTGCTGCACTCCACGTCCCCCTACCAGGGCTCCAGCCCCCAG  
GGAAATCTCCGACCAGGCCCGCCAGGAGCCAGATCCAGGCTCCTGGAAGAACCATGTCCGGC  
AGCTACTGGTCATGCCAGGCACACACTGCTGCCCAAGAGGAGCTGCTGTTGAATTATCTGTG  
AATGTTGGGAAGAGGAATGCCAGAGCTGCCGGCTGAAAATTACCCAACCAAGAGAAATCTGCAGG  
**ATGG**ACTTTCTGGTCCTCTTCTTGTCTACCTGGCTTCGGTGCTGATGGGTCTTGTTCCTTATC  
TGCGTCTGCTCGAAAACCCATAGCTTGAAAGGCCCTGGCCAGGGGAGGAGCACAGATATTTTCC  
TGTATAATTCCAGAATGTCTTCAGAGAGCCGTGCATGGATTGCTTCATTACCTTTTCCATACG  
AGAAACCACACCTTCATTGTCCTGCACCTGGTCTTGCAAGGGATGGTTTATACTGAGTACACC  
TGGGAAGTATTTGGCTACTGTCAGGAGCTGGAGTTGTCCTTGCAATTACCTTCTTCTGCCCTAT  
CTGCTGCTAGGTGTAAACCTGTTTTTTTTTACCCTGACTTGTGGAACCAATCCTGGCATTATA  
ACAAAAGCAAATGAATTATTATTTCTTCATGTTTATGAATTTGATGAAGTGATGTTTCCAAAG  
AACGTGAGGTGCTCTACTTGTGATTTAAGGAAACCAGCTCGATCCAAGCACTGCAGTGTGTGT  
AACTGGTGTGTGCACCGTTTCGACCATCACTGTGTTTGGGTGAACAACATGCATCGGGGCCTGG  
AACATCAGGTACTTCCTCATCTACGTCTTGACCTTGACGGCCTCGGCTGCCACCGTCGCCATT  
GTGAGCACCCTTTTCTGGTCCACTTGGTGGTGATGTCAGATTTATACCAGGAGACTTACATC  
GATGACCTTGGACACCTCCATGTTATGGACACGGTCTTTCTTATTCAGTACCTGTTCTGACT  
TTTCCACGGATTGTCTTCATGCTGGGCTTTGTGCTGGTTCTGAGCTTCCTCCTGGGTGGCTAC  
CTGTTGTTTGTCTGTATCTGGCGGCCACCAACCAGACTACTAACGAGTGGTACAGAGGTGAC  
TGGGCCTGGTGCCAGCGTTGTCCCTTGTGGCCTGGCCTCCGTCAGCAGAGCCCCAAGTCCAC  
CGGAACATTCACTCCCATGGGCTTCGGAGCAACCTTCAAGAGATCTTTCTACCTGCCTTTCCA  
TGTCATGAGAGGAAGAAACAAGAA**TGA**CAAGTGTATGACTGCCTTTG

587/615

**FIGURE 582**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA144857
><subunit 1 of 1, 344 aa, 1 stop
><MW: 39787, pI: 7.44, NX(S/T): 2
MDFLVLFYFLASVLMGLVLICVCSKTHSLKGLARGGAQIFSCIPECLQRAVHGLLHYL
FHTRNHTFIVLHLVLQGMVYTEYTWEVFGYCQELESLHYLLLPYLLLGVNLFFFTLTCG
TNPGIITKANELLFLHVYEFDEVMFPKNVRCSTCDLRKPARSKHCSVCNWCVHRFDHHCV
WVNNCIGAWNIRYFLIYVLTLTASAATVAIVSTTFLVHLVVMSDLYQETYIDDLGHLHVM
DTVFLIQYLFLLTFPRIVFMLGFVVVLSFLLGGYLLFVLYLAATNQTTNEWYRGDWAWCQR
CPLVAWPPSAEPQVHRNIHSHGLRSNLQEIFLPAFPCHERKKQE
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-29

**Transmembrane domains:**

Amino acids 100-116;201-217;256-275

**N-glycosylation sites:**

Amino acids 65-69;284-290

**N-myristoylation sites:**

Amino acids 32-38;77-83;120-126;322-328

**Cell attachment sequence:**

Amino acids 292-298

**DHHC zinc finger domain:**

Amino acids 140-204

588/615

**FIGURE 583**

CCGCGGAAGTGGCAGGCGTTTCAGAGCGTCAGAGGCTGCGGATGAGCAGACTTGGAGGACTCCAGGCCAGAGACT  
AGGCTGGGCGAAGAGTTCGAGCGTGAAGGGGGCTCCGGGCCAGGGTGACAGGAGGCGTGCTTGAGAGGAAGAAGTT  
GACGGGAAGGCCAGTTCGACGGCAAATCTCGTGAACCTTGGGGGACGAATGCTCAGGATGCGGGTCCCCGCCCTC  
CTCGTCCTCCTCTTCTGCTTCAGAGGGAGAGCAGGCCCCGTGCGCCCATTTCTGCAACAGCCAGAGGACCTGGTG  
GTGCTGCTGGGGGAGGAAGCCCGGCTGCCGTGTGCTCTGGGCGCCTACTGGGGGCTAGTTCACTGGACTAAGAGTGGG  
CTGGCCCTAGGGGGGCCAAAGGGACCTACCAGGGTGGTCCCGGTACTGGATATCAGGGAATGCAGCCAATGGCCAG  
CATGACCTCCACATTAGGCCCCGTGGAGCTAGAGGATGAAGCATCATATGAATGTCAAGGTACACAAGCAGGCCTC  
CGCTCCAGACCAGCCCAACTGCACGTGCTGGTCCCCCAGAAGCCCCCAGGTGCTGGGCGGCCCCCTCTGTGTCT  
CTGGTTGCTGGAGTTCTGCGAACCTGACATGTGCGAGCCGTGGGGATGCCCCGCCCTACCCCTGAATTGCTGTGG  
TTCCGAGATGGGGTCTGTGGATGGAGCCACCTTTTCATCAGACCCTGCTGAAGGAAGGGACCCCTGGGTCACTG  
GAGAGCACCTTAACCTGACCCCTTTTCAGCCATGATGATGGAGCCACCTTTGTCTGCCGGGCCCCGAGCCAGGCC  
CTGCCCACAGGAAGAGACACAGCTATCACACTGAGCCTGCAGTACCCCCAGAGGTGACTCTGTCTGCTTCGCCA  
CACACTGTGCAGGAGGGAGAGAAGGTCATTTTCTGTGCCAGGCCACAGCCCAGCCTCCTGTCAAGGCTACAGG  
TGGGCAAAAGGGGGCTCTCCGGTGTCTGGGGCCCCGCGGGCCAAGGTTAGAGGTCTGGGAGAGCGCTCGTTCCCTG  
ACTGAGCCCGTGTCTGCGAGGTGAGCAACGCCGTGGGTAGCGCCAACCGCAGTACTGCGCTGGATGTGCTGTTT  
GGGCCGATTCTGCAGGCAAAAGCCGGAGCCCGTGTCCGTGGACGTGGGGGAAGACGCTTCTTCAGCTGCGCCTGG  
CGCGGAACCCGCTTCCACGGGTAACCTGGACCCGCGCGGTGGCGCGCAGGTGCTGGGCTCTGGAGCCACACTG  
CGTCTTCCGTCCGTGGGGCCCCGAGGACGCGAGGCGACTATGTGTGCAGAGCTGAGGCTGGGCTATCGGGCCTGCGG  
GGCGGCGCGCGGAGGCTCGGCTGACTGTGAACGCTCCCCCAGTAGTGACCGCCCTGCACTCTGCGCCTGCGCTTC  
CTGAGGGGGCCCTGTCTGCGCTCCAGTGTCTGTTTTGCGCTCTCCCGCCCCAGATGCCGTGGTCTGGTCTTGGGAT  
GAGGGCTTCTGAGGCGGGGTGCGAGGGCCGTTTCTGGTGGAGACATTCCCTGCCCCAGAGAGCCGCGGGGGGA  
CTGGGTCCGGGCTGATCTCTGTGCTACACATTTCCGGGACCCAGGAGTCTGACTTTAGCAGGAGCTTTAACTGC  
AGTGCCCGGAACCGGCTGGGCGAGGGAGGTGCCAGGCCAGCCTGGGCGGTAGAGACTTGCTGCCCACTGTGCGG  
ATAGTGGCCGGAGTGGCCGCTGCCACCACAACCTCTCCTTATGGTCATCACTGGGGTGGCCCTCTGCTGCTGGCGC  
CACAGCAAGGCCTCAGCCTCTTTCTCCGAGCAAAAGAACCTGATGCGAATCCCTGGCAGCAGCGACGGCTCCAGT  
TCACGAGGTCTGAAGAAGAGGAGACAGGCAGCCGCGAGGACCGGGGCCCCATTGTGCACACTGACCACAGTGAT  
CTGGTTCTGGAGGAGGAAGGGACTCTGGAGACCAAGGACCAACCAACGGTTACTACAAGGTCCGAGGAGTCACT  
GTGAGCCTGAGCCTTGCGCAAGCCCCCTGGAGGAGGTCTCTTCTGCCACCAACCTCCCCCTTGGGCCCCCAGGG  
ACCCCTACCTTCTATGACTTCAACCCACACCTGGGCATGGTCCCCCCTGCAGACTTTACAGAGCCAGGGCAGGC  
TATCTACCCACACCCACCCCTCGAGCTTTCACAGCTACATCAAACCCACATCCTTTGGGCCCCCAGATCTGGCC  
CCCCGGGACTCCCCCTTCCCATATGCTGCTTCCCCACACCTAGCCACCCGCTCTCCAGACTCACGTGTGACAT  
CTTTCCAATGGAAGAGTCTCTGGGATCTCCAATTGCCATAATGGATTGTTCTGATTTCTGAGGAGCCAGGACAAG  
TTGGCGACCTTACTCCTCCAAACTGAACACAAGGGGAGGGAAAGATCATTACATTTGTCAAGGAGCATTGTATA  
CAGTCAGCTCAGCCAAAGGAGATGCCCCAAGTGGGAGCAACATGGCCACCCAATATGCCACCTATTCCCCGGTG  
TAAAAGAGATTCAAGATGGCAGGTAGGCCCTTTGAGGAGAGATGGGACAGGGCAGTGGGTGTTGGGAGTTTGGG  
GCCGGGATGGAAGTTGTTTCTAGCCACTGAAAGAAGATATTTCAAGATGACCATCTGCATTGAGAGGAAAGGTAG  
CATAGGATAGATGAAGATGAAGAGCATACAGGCCCCACCCCTGGCTCTCCCTGAGGGGAACTTTGCTCGGCCAAT  
GGAATGCAGCCAAGATGGCCATATACTCCCTAGGAACCAAAATGGCCACCATCTTGATTTTACTTTCCTTAAA  
GACTCAGAAAGACTTGGACCCAAGGAGTGGGGATACAGTGAGAATTACCACTGTTGGGGCAAAATATTGGGATAA  
AAATATTTATGTTTAATAATAAAAAAAGTCAAAGAGAAAAAAA

589/615

**FIGURE 584**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA145841
><subunit 1 of 1, 708 aa, 1 stop
><MW: 75093, pI: 6.65, NX(S/T): 3
MLRMRVPALLVLLFCFRGRAGSPHFLQOPEDLVVLLGEEARLPCALGAYWGLVQWTKSG
LALGGQRDLPGWSRYWISGNAANGQHDHLHIRPVELEDEASYECQATQAGLRSRPAQLHVL
VPPEAPQVLGGPSVSLVAGVPANLTCRSRGDARPTPELLWFRDGVLLDGATFHQTLLKEG
TPGSVESTLTLPFSHDDGATFVCRARSQALPTGRDTAITLSLQYPPEVTLSPHTVQE
GEKVIFLCQATAQPPVTGYRWAKGGSPVLGARGPRLEVVDASFLTEPVSCVSNVAVGSA
NRSTALDVLFGPILQAKPEPVSDVGEDASFSCAWRGNPLPRVTWTRRGAQVLGSGATL
RLPSVGPEDAGDYVCRAEAGLSGLRGGAEARLTVNAPPVVVALHSAPAFIRGPARLQCL
VFASPADAVVWSWDEGFLEAGSQGRFLVETFPAPESRGGGLGPGGLISVLHISGTQESDFS
RSFNCSARNRLGEGGAQASLGRRDLLPTVRIVAGVAAATTTLLMVITGVALCCWRHASKAS
ASFSEQNLMRIPGSSDGSRRGPEEEETGSREDRGPIVHTDHSDLVLEEEGTLETKDPT
NGYYKVRGVSLSLGEAPGGGLFLPPPSPLGPPGTPTFYDFNPHLGMVPPCRLYRARAG
YLTTPHPRAFTSYIKPTSFPGPDLAPGTPPFPYAAFTPSHPRLQTHV
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-20

**Transmembrane domain:**

Amino acids 511-531

**N-glycosylation sites:**

Amino acids 143-147;301-305;484-488

**N-myristoylation sites:**

Amino acids 48-54;60-66;79-85;139-145;180-186;183-189;355-361;383-389;  
387-393;460-466;473-479;494-500;495-501;514-520;528-534;  
554-560;592-598;608-614

**Amidation site:**

Amino acids 500-504

**Cell attachment sequence:**

Amino acids 149-152

**Multicopper oxidases signature 1:**

Amino acids 445-466

**Immunoglobulin domain:**

Amino acids 326-377

**FIGURE 585**

GCCCGCCTGAGGAAGCCGCTGTGCCTGGGATGCCAAGAGCCAGAGAATGGATCTTCTCCGAGTGGGGACATTGCTGACAATCCCGGCTTCCCGAGGCGGCTAAGAACAGGCAGTTTGTGTCTCGGCTGCTGCAGATACCCAGAGGCACAAAGAGACCGAAGCCACCCGGAGGGACCCACGGACGGACAGATGGTAGGCGCGAAACCCGAGAGGACCGGCGGAGGCTGAGCACCAGAGCCGCCAAGGAAGAGAACTAACCACAGCCAAAGTTACCCCGCCGGCTTTCCTTCGCTGCGCTAAGGAATGAACCCTTCCAGCTCGATCTGCTCTTCGTCTGCTTCTTCCTCTTCAGTCAAGAGCTGGGCCTCCAGAAGAGAGGATGCTGTCTGGTGTCTGGGCTACATGGCCAAGGACAAGTTTCGGAGAATGAATGAAGGCCAAGTCTATTTCCTTCAGCCAGCAGCCCCAGGACCAGGTGGTGGTGTCTGGGACAGCCAGTGACGCTACTTTGCGCCATCCCCGAATACGATGGCTTCGTTCTGTGGATCAAGGACGGCTTGGCTCTGGGTGTGGGCAGGGACCTCTCAAGTTACCCACAGTACCTGGTGGTAGGGAACCACTGTCTAGGGGAGCACACCTGAAGATCCTGAGGGCAGAGCTGCAAGACGATGCGGTGTACGAGTGCCAGGCCATCCAGGCCGCTATCCGCTCCCGCCCCGCACGCCTCACAGTCTTGGTGCCGCTGATGACCCCGTCTATCTGGGGGGCCCTGTGATCAGCCTGCGTGCGGGGGACCTCTCAACCTCACCTGCCACGCAGACAATGCCAAGCCTGCAGCCTCCATCATCTGGTTGCGAAAGGGAGAGGTCATCAATGGGGCCACTACTCCAAGACCTGCTTCGGGACGGCAAGCGGGAGAGCATCGTCAGCACCCCTCTTCATCTCCCTGGTGACGTGGAGAATGGCCAGAGCATCGTGTGTCTGTCGCCACCAACAAAGCCATCCCCGAGGAAAGGAGACGTCGGTCACCATTGACATCCAGCACCCCTCCACTGGTCAACCTCTCGGTGGAGCCACAGCCAGTGCTGGAGGACAACGTGCTCACTTTCCACTGCTCTGCAAAGGCCAACCCAGCTGTCACCAGTACAGGTGGGCCAAGCGGGGCCAGATCATCAAGGAGGCATCTGGAGAGGTGTACAGGACCACAGTGGACTACACGTACTTCTCAGAGCCCGTCTCCTGTGAGGTGACCAACGCCCTGGCAGCACCAACCTCAGCCGCACGGTTGACGTCTACTTTGGGCCCCGGATGACCACAGAACCACAATCCTTGCTCGTGGATCTGGGCTCTGATGCCATCTTCAGCTGCGCCTGGACCGGCAACCCATCCCTGACCATCGTCTGGATGAAGCGGGGCTCCGGAGTGGTCTGAGCAATGAGAAGACCCTGACCCTCAAATCCGTGCGCCAGGAGGACGCGGGCAAGTACGTGTGCCGGGCTGTGGTGCCCCGTGTGGGAGCCGGGGAGAGAGAGAGGTGACCCTGACCGTCAATGGACCCCCCATCATCTCCAGCACCAGACCCAGCACGCCCTCCACGGCGAGAAGGGCCAGATCAAGTGCTTCATCCGGAGCACGCCGCCGCCGGACCGCATCGCCTGGTCTTGGAAAGGAGAACGTTCTGGAGTCGGGCACATCGGGGCGGTATACGGTGGAGACCATCAGCACCGGAGGGCGTCATCTCCACCCTGACCATCAGCAACATGTGCGGGCCGACTTCCAGACCATCTACAACCTGCACGGCCTGGAACAGCTTCGGCTCCGACACTGAGATCATCCGGCTCAAGGAGCAAGGTTTCGGAAATGAAGTCGGGAGCCGGGCTGGAAGCAGAGTCTGTGCCGATGGCCGTTCATATTGGGGTGGCCGTAGGAGCTGGTGTGGCCTTCTCTGTCCTATGGCAACCATCGTGGCGTTCTGCTGTGCCCGTTCCAGAGAAGTACGGGAGGGAGATCCGGATCTCAGGGAGGGGACAGAGAAAAAGGCCAGGCTTAGGCTGCCCCGGAGAGCAAGTAAGCAGAGTGCAATGAACAGGGGTCTTAAACAGTGCTGTGAGCTCCTGGGGCAGGGAGTGGGTCTGATGCATCGGTGTATGTGAGCCTGGGCAACATGGCGCCTGGCAGAGTGGGCGCTAGGCTGAGGTTGACCTGGACTAGACTGAACCTTCAGTCTGCAGGGCAGCCAGCATTTTGATTGAACACATAGCTCTTCAGTCAGGAACTGTACAGAAAGATAGGGGGGAAAGCGGTTTGTGGTTTGATCCTTGCTCTACAAGAGCTGTTAGTCTAGAGAGACCCCATCTCTACAACAAAATAAAAATAAAGAGCTGCTAGTCTACCAGAAAAGCAGGTCACCTCACACAGCTGTGGGGGAGTGGGTGGGGAAGCAATAAAGGAATGCTTTTGAGAAAACCTTAA

591/615

**FIGURE 586**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA148004
><subunit 1 of 1, 600 aa, 1 stop
><MW: 65308, pI: 8.35, NX(S/T): 5
MKPFQLDLLFVCFLLFSQELGLQKRGCCLVLGMAKDKFRRMNEGQVYSFSQQPQDQV
SGQPVTLTLLCAIPEYDGFVLWIKDGLALGVGRDLSSYPQYLVVGNHLSGEHHLKILRAELQ
DDAVYECQAIQAIRSRPARLTVLVPPDDPVILGGPVISLRAGDPLNLTCHADNAKPAAS
IIWLRKGEVINGATYSKTLRLDGKRESIVSTLFI SPGDVENGQSIVCRATNKAI PGGKET
SVTIDIQHPPLVNLVSEVPQPVLEDNVVTFHCSAKANPAVTQYRWAKRGQIIKEASGEVYR
TTVDYTYFSEPVSCVTNALGSTNLSRTVDVYFGPRMTTEPQSLLDLGSDAIFSCAWTG
NPSLTIVWMKRGSGVLSNEKTLTLKSVRQEDAGKYVCRAVVPRVGAGEREVTTLTVNGPP
IISSTQTQHALHGEKGQIKCFIRSTPPPDRIAWSWKENVLESSTSGRYTVETISTEEGVI
STLTISNIVRADFQTIYNCTAWNSFGSDTEIIRLKEQGSEMKGAGLEAESVPMMAVIIGV
AVGAGVAFLVLMATIVAFCCARSQRSTGGRSGISGRGTEKKARLRLPRASKQECNEQGS
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-17

**Transmembrane domain:**

Amino acids 534-555

**N-glycosylation sites:**

Amino acids 167-171;253-257;324-328;498-502

**Glycosaminoglycan attachment sites:**

Amino acids 523-527;574-578

**cAMP- and cGMP-dependent protein kinase phosphorylation sites:**

Amino acids 204-208;370-374;588-592

**Tyrosine kinase phosphorylation sites:**

Amino acids 40-49;300-308;389-397

**N-myristoylation sites:**Amino acids 45-51;62-68;84-90;103-109;192-198;236-242;  
374-380;436-442;478-484;539-545;543-549;  
568-574**Amidation site:**

Amino acids 202-206

**Leucine zipper pattern:**

Amino acids 8-30

592/615

**FIGURE 587**

CAAAAAAGGAGCATGTCTTCATCCATGAGAGGCCTCGAAAAATCAATGGTATTTGCATTTCTC  
CCAAGAAGGTTGCTTGCCAAAACCTTTTCGGCCATTTTCTGCTTTCAGAGTGAGACAAAGTTCA  
AAATGACAGTCTGTCAGCTCATTGAAGGCACTAGATACCCTGCCTGCAGGTACCACTATTCCC  
CCACAGAGGGGTTTTGTTCTTGTCACTTGTGATGACTTGAGGCCAGATAGTTTCTTGGCTATG  
TTAAATAACTCAAGATCAGCTACCGAGTCTGAGATCTCTTCTCTCATGGCATTGGAGCTGGCT  
GTGCCTGAGGCAGACCTGGACCGTGGACATGGGGCAATGCCTTGAGCGGAAGGGGAAGCCACT  
GAATTTTGGGTGTCACCAGGTAAACAGAGCCCTCAGCATCTGAATAGAACTGAACAGGAACA  
GAAGAGATTACACTACATCTGAGATGGAGACCTTTCCTCTGCTGCTGCTCAGCCTGGGCCTGG  
TTCTTGCAGAAGCATCAGAAAGCACAATGAAGATAATTAAAGAAGAATTTACAGACGAAGAGA  
TGCAATATGACATGGCAAAAAGTGGCCAAGAAAAACAGACCATTGAGATATTAATGAACCCGA  
TCCTGTTAGTTAAAAATACCAGCCTCAGCATGTCCAAGGATGATATGTCTTCCACATTACTGA  
CATTGAGAAGTTTACATTATAATGACCCCAAGGGAAACAGTTCGGGTAATGACAAAGAGTGTT  
GCAATGACATGACAGTCTGGAGAAAAGTTTCAGAAGCAAACGGATCGTGCAAGTGGAGCAATA  
ACTTCATCCGCAGCTCCACAGAAGTGATGCGCAGGGTCCACAGGGCCCCCAGCTGCAAGTTTGTA  
CAGAATCCTGGCATAAGCTGCTGTGAGAGCCTAGAAGTGGAAAATACAGTGTGCCAGTTCACT  
ACAGGCAAACAATTCCCCAGGTGCCAATACCATAGTGTTACCTCATTAGAGAAGATATTGACA  
GTGCTGACAGGTCATTCTCTGATGAGCTGGTTAGTTTGTGGCTCTAAGTTGTAAATCCCACAG  
AGCTTTAGGACTAGGGTCTTACTAAAGAAGGACCTCTTCTTGTTTCATTCTTGTTTAAACCTTT  
CCTTAATATCTACTCTTTAGCACTATAGTGAACCTCTGATTATTTATTCTAACTGGAGGAGTG  
AAAAATCCAAAATTGTGGATAATTCAATTAAAAGTTATGACTGATACCG

593/615

**FIGURE 588**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA149893
><subunit 1 of 1, 199 aa, 1 stop
><MW: 22427, pI: 6.46, NX(S/T): 3
METFPLLLLSLGLVLAEESESTMKIIKEEFTDEEMQYDMAKSGQEKQTIEILMNPILLVK
NTSLSMSKDDMSSTLLTFRSLHYNDPKGNSGNDKECCNDMTVWRKVSEANGSCKWSNNF
IRSSTEVMRRVHRAPSCKFVQNPGISCCESLELENTVCQFTTGKQFPRCQYHSVTSLEKI
LTVLTGHSLSMSWLVCCKSL
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-16

**N-glycosylation sites:**

Amino acids 61-65;89-93;111-115

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 105-109

**N-myristoylation sites:**

Amino acids 12-18;88-94;144-150

**Microbodies C-terminal targeting signal:**

Amino acids 197-201



594/615

**FIGURE 589**

CAGTCCTGCCGGGACGGTGAGCGCATTTCAGCACCCCTGGACAGCACCGCGGTTGCGCTGCCTCC  
AGGGCGGCCCCGGGCTGCTCCTGCTCCGCAGAGCTACGCCCTCCCCCGGGTGCCCCGGACCC  
TGCACTTGCCGCGCTTTCTCGCGCTGCTCTGGACCTTGCTAGCCGGCTCTGCACCTCCCAG  
AAGCCGTGGGCGCGCCGCTCAGCTGCTCCATCGCCTCACTTTCCCAGGCTCGCGCCCCGAAGCA  
GAGCCATGAGAACCCCAGGGTGCTGGCGAGCCGCTAGCGCCATGGGGCCCCGGCGAGGCGCTG  
CTGGCGGGTCTCCTGGTGATGGTACTGGCCGTGGCGCTGCTATCCAACGCACTGGTGCTGCTT  
TGTTGCGCTACAGCGCTGAGCTCCGCACTCGAGCCTCAGGCGTCCTCCTGGTGAATCTGTCT  
CTGGGCCACCTGCTGCTGGCGGCGCTGGACATGCCCTTCACGCTGCTCGGTGTGATGCGCGGG  
CGGACACCGTCGGCGCCCCGGCGCATGCCAAGTCATTGGCTTCCTGGACACCTTCCTGGCGTCC  
AACGCGGCGCTGAGCGTGGCGGCGCTGAGCGCAGACCAGTGGCTGGCAGTGGGCTTCCCCTG  
CGCTACGCCGGACGCTGCGACCGCGCTATGCCGGCCTGCTGCTGGGCTGTGCCTGGGGACAG  
TCGCTGGCCTTCTCAGGCGCTGCACTTGGCTGCTCGTGGCTTGGCTACAGCAGCGCCTTCGCG  
TCCTGTTGCTGCGCCTGCCGCCCCGAGCCTGAGCGTCCGCGCTTCGCAGCCTTCACCGCCACG  
CTCCATGCCGTGGGCTTCGTGCTGCCGCTGGCGGTGCTCTGCCTCACCTCGCTCCAGGTGCAC  
CGGGTGGCACGCAGACACTGCCAGCGCATGGACACCGTCACCATGAAGGCGCTCGCGCTGCTC  
GCCGACCTGCACCCCAGTGTGCGGCAGCGCTGCCTCATCCAGCAGAAGCGGCGCCGCCACCGC  
GCCACCAGGAAGATTGGCATTGCTATTGCGACCTTCCTCATCTGCTTTGCCCCGTATGTCATG  
ACCAGGCTGGCGGAGCTCGTGCCCTTCGTACCGTGAACGCCAGTGGGGCATCCTCAGCAAG  
TGCCTGACCTACAGCAAGGCGGTGGCCGACCCGTTACGTA CTCTGCTCCGCCGGCCGTTTC  
CGCCAAGTCCTGGCCGGCATGGTGCACCGGCTGCTGAAGAGAACCCCGCGCCCAGCATCCACC  
CATGACAGCTCTCTGGATGTGGCCGGCATGGTGCACCACTGCTGAAGAGAACCCCGCGCCCA  
GCGTCCACCCACAACGGCTCTGTGGACACAGAGAATGATTCTGCTGCCTGCAGCAGACACACTGA  
GGGCTGGCAGGGCTCATCGCCCCACCTTCTAAGAAGCCCTGTGGAAAGGGCACTGGCCCTG  
CCACAGAGATGCCACTGGGGACCCCCAGACACCAGTGGCTTGACTTTGAGCTAAGGCTGAG

595/615

**FIGURE 590**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA149930
><subunit 1 of 1, 363 aa, 1 stop
><MW: 39332, pI: 10.42, NX(S/T): 3
MGPGEALLAGLLVMVLAVALLSNALVLLCCAYS AELRTRASGVLLVNL SLGHLLLAALDM
PFTLLGVMRGRTPSAPGACQVIGFLDTFLASNAALSVAALSADQWLAVGFPLRYAGRLRP
RYAGLLLGCAWGQSLAFSGAALGCSWLGYSSAFASCSLRLPPEPERPRFAAFTATLHAVG
FVLPLAVLCLTSLQVHRVARRHCQRM DTVTMKALALLADLHPSVRQRCLIQKRRRRHRAT
RKIGIAIATFLICFAPYVMTRLAELVPFVTVNAQWGILSKCLTYSKAVADPFTYSLLRRP
FRQVLAGMVHRL LKRTPRPASTHDSSLDVAGMVHQLLKRTPRPASTHNGSVDTENDSCLQ
QTH
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-24

**Transmembrane domains:**

Amino acids 46-60;85-103;130-150;175-192;246-264

**N-glycosylation sites:**

Amino acids 47-51;348-352;355-359

**Tyrosine kinase phosphorylation site:**

Amino acids 286-295

**N-myristoylation sites:**Amino acids 66-72;124-130;128-134;132-138;139-145;244-250;  
349-355**G-protein coupled receptor proteins:**

Amino acids 72-112

**7 transmembrane receptor (rhodopsin family):**

Amino acids 22-294

596/615

**FIGURE 591**

AACATGGCTGCGGCGCCTGGGCTGCTCGTCTGGCTGCTCGTCCGGCTGCCCTGGCGGGTG  
CCGGGCCAGCTGGACCCCAGCACTGGCCGGCGGTTCTCGGAGCACAACTCTGCGCGGACGAC  
GAATGCAGCATGATGTACCGCGGTGAGGCTCTTGAAGATTTACAGGCCCGGATTGTCGTTTT  
GTGAATTTTAAAAAAGGTGATCCTGTATATGTTTACTATAAACTGGCAAGAGGATGGCCTGAA  
GTTTGGGCTGGAAGTGTTGGACGCACTTTTGGATATTTTCCAAAAGATTTAATCCAGGTAGTT  
CATGAATATACCAAAGAAGAGCTACAAGTTCCAACAGATGAGACGGATTTTGTTTGTGTTTGAT  
GGAGGAAGAGATGATTTTTCATAATTATAATGTAGAAGAAGCTTTTAGGGTTTTTGGAACGTAC  
AATTCTGCAGCTACAGATTCTGAGAAAGCTGTAGAAAAAAGCTTTACAGGATATGGAAAAAAC  
CCTGAATTATCTAAGGAAAGGGAACCTGAACCTGAACCAGTAGAAGCCAACCTCAGAGGAAAGT  
GATAGTGTATTCTCAGAAAAACTGAGGATCTTCAGGAACAGTTTACAACCTCAGAAGCACCAC  
TCCCATGCAACAGCCAAGCAAATCATGCTCAGGGAGAGCAGGCTTCATTTGAATCTTTTGAA  
GAAATGCTGCAAGATAAACTAAAAGTGCCAGAAAGTGAAAACAACAAACCAGCAATAGTTCT  
CAGGTCTCAAATGAACAGGATAAGATTGATGCCTATAAACTTTTGAAAAAGAAATGACTCTA  
GACTTGAAAACCAAATTTGGCTCAACAGCTGATGCCTTGATCTGATGATGAGACAACCAGA  
CTCGTTACTTCATTAGAAGATGATTTTGATGAGGAATTGGATACTGAGTATTATGCAGTTGGA  
AAGGAAGATGAGGAGAACCAAGAAGACTTTGATGAGTTGCCATTACTTACCTTTACAGATGGG  
GAAGATATGAAAACCTCAGCAAAGTCTGGCGTTGAGAAATATCCAACAGATAAAGAGCAGAAT  
TCAAATGAAGAGGACAAGGTTCAAGCTAAGTGTGCCCCCTGGCATCAAAAATGATGATAAAAT  
ATACTAACAACCTGGGGGGACACTATCTTCTCTATTGTACAGGAGGTGAAGAAACAAGAGAT  
ACGATGGATTTAGAGAGCTCTAGTTCAAGAGGAAGAAAAAGAGATGATGATGATGCATTAGTC  
CCAGATAGCAAACAGGGGAAACCACAGTCAGCAACAGATTATAGTGACCCTGACAATGTAGAT  
GATGGTCTTTTTTATTGTAGACATTCCTAAAACAAATAATGACAAAGAAGTAAACGCAGAACAT  
CACATTAAAGGAAAAGGGAGGGGAGTTCAAGGAATCCAAGAGGGGCCTGGTACAAGATGAGACA  
GAATTAGAGGATGAAAATCAAGAAGGCTTTAAACAGAGCCCATAAACTATGACCTCTGAGG  
TTTCATTGGAAAGAAAGTGTACTGTGCATTATCCATTACAGTAAAGGATTTTCATTGGCTTCAA  
AATCCAAAAGTTTATTTTAAAAGGTTTGTTGTTAGAACTAAGCTGCCTTGGCAGTGTGCATTT  
TTGAGCCAAACAATTCAAAAATGTCATTTCTCCCTAAATAAAAATCACCTTTTAAGCTAGAG  
CGTCCTTACAACCTTTGAAATGTGCAATAAAGAATACCTGTGTTTTAGCTAATGTAGCATATGT  
AATTGCAAATGATTTAGAATGTCATGAAAAATATGAACATTTCTGTGGAAATGCTTTAAGA  
ACATGTATTTCCATTATCCTATTTTGTAGTACACCAGCTGAATACGGAGCAATGGTGTGTTAT  
AAGCGTTTTTTTAACTATCTGGTCACAAAGACTGTTACGCTAAAAATGTTTACTAAAAGATC  
ACTAACTATCTCCCCTCTTGCTGAAGTTCTTTGTAGTAATAGCTCATAAAAATTTGTTTATT  
AATATTTAAAAA

597/615

**FIGURE 592**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA150157.  
><subunit 1 of 1, 499 aa, 1 stop  
><MW: 56471, pI: 4.31, NX(S/T): 2  
MAAAPGLLVWLLVLRLLPWRVPGQLDPSTGRRFSEHKLCADDECSMMYRGEALEDFTGPDC  
RFVNFKKGDPVYVYYKLARGWPEVWAGSVGRTFGYFPKDLIQVVHEYTKHEELQVPTDETD  
FVCFDGGRRDDFHNYNVEELLGFLELYNSAATDSEKAVEKTLQDMEKNPELSKEREPEPEP  
VEANSEESDSVFSENTEDLQEQFTTQKHHSHANSQANHAQGEQASFESFEEMLQDKLKVP  
ESENKTSNSSQVSNEQDKIDAYKLLKKEMTLDLKTKFGSTADALVSDDETTRLVTSLED  
DFDEELDTTEYYAVGKEDEENQEDFDELPLLTFTDGEDMKTPAKSGVEKYPTDKEQNSNEE  
DKVQLTVPPGIKNDDKNILTTWGDITFSIVTGGEETRDMDLESSSSEEEKEDDDDALVP  
DSKQGKPQSATDYSDDPNVDDGLFIVDIPKTNNDKEVNAEHHIKGKGRGVQESKRGLVQD  
ETELEDENQEGFKTEPIKL
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-22

**N-glycosylation sites:**

Amino acids 245-249;249-253

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 30-34

**Tyrosine kinase phosphorylation site:**

Amino acids 66-72

**N-myristoylation sites:**

Amino acids 392-398;469-475

**Amidation site:**

Amino acids 28-32

**Aminoacyl-transfer RNA synthetases class-II signature 1:**

Amino acids 47-70

598/615

**FIGURE 593**

GGGCCAGTAGAGTGTGTCTGGGTCAGCTGAGTGACTACATCAAAGCTCCCAGCCTTGAAAAAC  
ACATGCTGTTCCAGGCTCAAGATATTGAAACATTAATTAGATAATTTAAAGTAGCGTTTTTC  
TTCTACAATGTCTGAAGAAGTGACCTACGCGACACTCACATTTCAGGATTCTGCTGGAGCAAG  
GAATAACCGAGATGGAAATAACCTAAGAAAAAGAGGGCATCCAGCTCCATCTCCCATTTGGCG  
TCATGCTGCTCTGGGTCTGGTAACTCTTGCCTGATGTTGCTGATTGGGCTGGTGACGTTGGG  
GATGATGTTTTTGCAGATATCTAATGACATTAACCTCAGATTCAGAGAAATTGAGTCAACTTCA  
GAAAACCATCCAACAGCAGCAGGATAACTTATCCCAGCAACTGGGCAACTCCAACAACCTTGTC  
CATGGAGGAGGAATTTCTCAAGTCACAGATCTCCAGTCTACTGAAGAGGCAGGAACAAATGGC  
CATCAAACCTGTGCCAAGAGCTAATCATTCTACTTTCAGACCACAGATGTAATCCATGTCCTAA  
GATGTGGCAATGGTACCAAAATAGTTGCTACTATTTTACAACAAATGAGGAGAAAACCTGGGC  
TAACAGTAGAAAGGACTGCATAGACAAGAAGCTCCACCCTAGTGAAGATAGACAGTTTGAAGA  
AAAGGATTTTCTTATGTCACAGCCATTACTCATGTTTTTCGTTCTTTTGGCTGGGATTATCATG  
GGACTCCTCTGGCAGAAGTTGGTTCTGGGAAGATGGCTCTGTTCCCTCTCCATCCTTGTACGT  
CTCTAACTATTGAGGGTAAACACAAGCTTTCCATGGAATCCTGGGAAAATTAATAATGATTGT  
GAGAATTATAAATACAGACATAAAAAGAGGAGTACAACATACTGAGAAAAGAGCTCCAGTAAC  
AAATATTGAAAGGAGATTTAGTACTAAAGAAGCTTGACCAGATCAATGGATCCAAAGGATGTGC  
TTATTTTCAAAAAGGAAATATTTATATTTCTCGCTGTAGTGCTGAAATTTTTTGGATTTGCGA  
GAAGACAGCTGCCCCAGTGAAGACTGAGGATTTGGATTAGTATGCTTCTTCCAAATTCTCCAA  
GAAGTAAGAGACTTGTGAGTAAGCTCATATGAGGAAAGAGGAACTACGGTACCAGAGCAAGG  
GCGAATTCTGCA

599/615

**FIGURE 594**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA150163
><subunit 1 of 1, 232 aa, 1 stop
><MW: 26754, pI: 5.80; NX(S/T): 3
MSEEVTYATLTFQDSAGARNNRDGNLNRKRGHPAPSPIWRHAALGLVTLCLMLLIGLVTL
GMMFLQISNDINS DSEKLSQLQKTIQQQQDNLSQQLGNSNNLSMEEEFLLKSQISSLLKRQ
EQMAIKLCQELIIHTSDHRCNCPKMWQWYQNSCYFFTTNEEKTWANSRKDCIDKNSTLV
KIDSLEEKDFLMSQPLLMSFFWLGLSWDSSGRSWFWEDGSVPSPSLYVSNY
```

**Important features of the protein:****Transmembrane domain:**

Amino acids 42-62

**N-glycosylation sites:**

Amino acids 91-95;101-105;176-180

**N-myristoylation sites:**

Amino acids 17-23;97-103

600/615

**FIGURE 595**

CGGACGCGTGGGGAAGAGGAGGAGGAGGAAGAAGACGTGGACAAGGACCCCCATCCTACCCAG  
AACACCTGCCTGCGCTGCCGCCACTTCTCTTTAAGGGAGAGGAAAAGAGAGCCTAGGAGAACC  
**ATG**GGGGGCTGCGAAGTCCGGGAATTTCTTTTGCAATTTGGTTTCTTCTTGCTATGCTGACA  
GCGTGGCCAGGCGACTGCAGTCACGTCTCCAACAACCAAGTTGTGTTGCTTGATACAACAAC  
GTACTGGGAGAGCTAGGATGGAAAACATATCCATTAAATGGGTGGGATGCCATCACTGAAATG  
GATGAACATAATAGGCCCCATTCACACATACCAGGTATGTAATGTAATGGAACCAACCAAAAC  
AACTGGCTTCGTACAAACTGGATCTCCCGTGATGCAGCTCAGAAAATTTATGTGGAAATGAAA  
TTCACACTAAGGGATTGTAACAGCATCCCATGGGTCTTGGGGACTTGCAAAGAAACATTTAAT  
CTGTTTTATATGGAATCAGATGAGTCCCAACGGAATTAAATTCAGCCAAACCAGTATACAAAG  
ATCGACACAATTGCTGCTGATGAGAGTTTTACCCAGATGGATTTGGGTGATCGCATCCTCAA  
CTCAACACTGAAATTCGTGAGGTGGGGCCTATAGAAAGGAAAGGATTTTATCTGGCTTTTCAA  
GACATTGGGGCGTGCATTGCCCTGGTTTCAGTCCGTGTTTTCTACAAGAAATGCCCTTCACT  
GTTTCGTAACCTGGCCATGTTTCCTGATACCATTCOAAGGGTTGATTCCTCCTCTTTGGTTGAA  
GTACGGGGTTCTTGTGTGAAGAGTGCTGAAGAGCGTGACACTCCTAAACTGTATTGTGGAGCT  
GATGGAGATTGGCTGGTTCCTCTTGGAAGGTGCATCTGCAGTACAGGATATGAAGAAATTGAG  
GGTCTTGCCATGGAGCCTCCAAAGGCCGCTGCTTCT**TAG**TTGGCCATCTTGGCCCCACCCCGA  
AACAGTAACCTTTGAAGAATAAAAGAAAAAGCAAAAGAGTAGCATTACTAAAATATTAAACGG  
TTACATTTACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

601/615

**FIGURE 596**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA153579
><subunit 1 of 1, 285 aa, 1 stop
><MW: 32368, pI: 5.32, NX(S/T): 0
MGGCEVREFLLQFGFFLPMLTAWPGDCSHVSNNQVVLLDTTTVLGELGWKTYPLNGWDAI
TEMDEHNRPIHTYQVCNVMEPNQNNWLRTNWI SRDAAQKIYVEMKFTLRDCNSIPWVLGT
CKETFNLFYMESESHGIKFKPNQYTKIDTIAADESFTQMDLGDRILKLNTEIREVGPIE
RKGFYLA FQDIGACIALVSVRVFYKKCPFTVRNLAMFPDTIPRVDSSSLVEVRGSCVKSA
EERDTPKLYCGADGDWLVLPLGRCICSTGYEEIEGSCHGASKGRCF
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-22

**N-myristoylation sites:**

Amino acids 192-198;274-280;278-284

**Receptor tyrosine kinase class V signature 1:**

Amino acids 192-209

**Ephrin receptor ligand binding domain:**

Amino acids 34-207



602/615

**FIGURE 597**

ACACTGGCCAAACAAAAACGAAAGCACTCCGTGCTGGAAGTAGGAGGAGAGTCAGGACTCCCA  
GGACAGAGAGTGCACAACTACCCAGCACAGCCCCCTCCGCCCCCTCTGGAGGCTGAAGAGGG  
ATTCCAGCCCCCTGCCACCCACAGACACGGGCTGACTGGGGTGTCTGCCCCCTTGGGGGGGGG  
CAGCACAGGGCCTCAGGCCTGGGTGCCACCTGGCACCTAGAAGATGCTGTGCCCTGGTTCTT  
GCTGTCTTGGCACTGGGCCGAAGCCAGTGGTCCTTTCTCTGGAGAGGCTTGTGGGGCCTCA  
GGACGCTACCCACTGCTCTCCGGGCCTCTCCTGCCGCCTCTGGGACAGTGACATACTCTGCCT  
GCCTGGGGACATCGTGCTGCTCCGGGCCCCGTGCTGGCGCCTACGCACCTGCAGACAGAGCT  
GGTGTGAGGTGCCAGAAGGAGACCGACTGTGACCTCTGTCTGCGTGTGGCTGTCCACTTGGC  
CGTGCATGGGCACTGGGAAGAGCCTGAAGATGAGGAAAAGTTTGAGGAGCAGCTGACTCAGG  
GGTGGAGGAGCCTAGGAATGCCTCTCTCCAGGCCCAAGTCGTGCTCTCCTTCCAGGCCTACCC  
TACTGCCCGCTGCGTCTGCTGGAGGTGCAAGTGCCTGCTGCCCTTGTGCAGTTTGGTCAGTC  
TGTGGGCTCTGTGGTATATGACTGCTTCGAGGCTGCCCTAGGGAGTGAGGTACGAATCTGGTC  
CTATACTCAGCCAGGTACGAGAAGGAACCTCAACCACACACAGCAGCTGCCTGCCCTGCCCTG  
GCTCAACGTGTCAGCAGATGGTGACAACGTGCATCTGGTTCTGAATGTCTCTGAGGAGCAGCA  
CTTCGGCCTCTCCCTGTACTGGAATCAGGTCCAGGGCCCCCCCCAAAACCCCGGTGGCACAAAAA  
CCTGACTGGACCGCAGATCATTACCTTGAACCACACAGACCTGGTTCCCTGCCTCTGTATTCA  
GGTGTGGCCTCTGGAACCTGACTCCGTTAGGACGAACATCTGCCCCCTCAGGGAGGACCCCCG  
CGCACACCAGAACCTCTGGCAAGCCGCCGACTGCGACTGCTGACCCTGCAGAGCTGGCTGCT  
GGACGCACCGTGCTCGCTGCCCGCAGAAGCGGCACTGTGCTGGCGGGCTCCGGGTGGGGACCC  
CTGCCAGCCACTGGTCCCACCGCTTTCTGAGGAAACGTCACTGTGGACAAGGTTCTCGAGTT  
CCCATTGCTGAAAGGCCACCCTAACCTCTGTGTTTCAAGGTGAACAGCTCGGAGAAGCTGCAGCT  
GCAGGAGTGCTTGTGGGCTGACTCCCTGGGGCCTCTCAAAGACGATGTGCTACTGTTGGAGAC  
ACGAGGCCCCCAGGACAACAGATCCCTCTGTGCCTTGGAAACCCAGTGGCTGTACTTCACTACC  
CAGCAAAGCCTCCACGAGGGCAGCTCGCCTTGGAGAGTACTTACTACAAGACCTGCAGTCAGG  
CCAGTGTCTGCAGCTATGGGACGATGACTTGGGAGCGCTATGGGCCTGCCCCATGGACAAATA  
CATCCACAAGCGCTGGGCCCTCGTGTGGCTGGCCTGCCTACTCTTTGCCGCTGCGCTTTCCCT  
CATCCTCCTTCTCAAAAAGGATCACGCGAAAGGGTGGCTGAGGCTCTTGAAACAGGACGTCCG  
CTCGGGGGCGGCCGCCAGGGGCCGCGCGGCTCTGCTCCTCTACTCAGCCGATGACTCGGGTTT  
CGAGCGCCTGGTGGGGCCTTGGCGTGGGCCCTGTGCCAGCTGCCGCTGCGCGTGGCCGTAGA  
CCTGTGGAGCCGTGCTGAACTGAGCGCGCAGGGGCCCGTGGCTTGGTTTACGCGCAGCGGCG  
CCAGACCCTGCAGGAGGGCGGCGTGGTGGTCTTGCTCTTCTCTCCGGTGCGGTGGCGCTGTG  
CAGCGAGTGGCTACAGGATGGGGTGTCCGGGCCCGGGGCGCACGGCCCGCACGACGCCTTCCG  
CGCCTCGCTCAGCTGCGTGCTGCCCCGACTTCTTGACAGGGCCGGGCGCCCGGACGTACGTGGG  
GGCCTGCTTCGACAGGCTGCTCCACCCGACGCGGTACCCGCCCTTTTCCGCACCGTGCCCGT  
CTTCACACTGCCCTCCCAACTGCCAGACTTCTTGGGGGCCCTGCAGCAGCCTCGCGCCCCGCG  
TTCCGGGGCGGCTCCAAGAGAGAGCGGAGCAAGTGTCCCGGGCCCTTCAGCCAGCCCTGGATAG  
CTACTTCCATCCCCCGGGGACTCCCGCGCCGGGACGCGGGGTGGGACCAGGGGCGGGACCTGG  
GGCGGGGGACGGGACTTAAATAAAGGCAGACGCTGTTTTTCTAAAAAA

603/615

**FIGURE 598**

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA164625
><subunit 1 of 1, 705 aa, 1 stop
/><MW: 76970, pI: 6.00, NX(S/T): 9
MPVPWFLLSLALGRSPVVLRLVGPQDATHCSPGLSCRLWDSILCLPGDIVPAPGP
VLAPTHLQTELVLRCKETDCDLCLRVAVHLAVHGHWEPEDEEKFGGAADSGVEEPRN
ASLQAQVVLSFQAYPTARCVLLEVQVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYT
QPRYEKELNHTQQLPALPWLNVSADGDNVHLVNLVSEEQHFGLSLYWNQVQGPPKPRWH
KNLTGPPQIITLNHTDILVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLRLT
LQSWLLDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPLLKGHPNLCV
QVNSSEKLQLOECLWADSLGPLKDDVLLLETRGPQDNRSLEPSGCTSLPSKASTRA
ARLGEYLLQDLQSGQCLQWLDDDLGALWACPMCKYIHKRWALVWLACLLFAAALSLILL
LKKDHAKGWLRLLLKQDVRSGAAARGRAALLYSADDSGFERLVGALASALCQLPLRVAV
DLWSRRELSAQGPVAFWHAQRRQTLQEGGVVLLFSPGAVALCSEWLQDGVSGPGAHGP
HDAFRASLSCVLPDFLQGRAPGSYVGACFDRLHPDAVPALFRTVPVFTLPSQLPDFLG
ALQQPRAPRSGRLQERAEQVSRAALQPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-20

**Transmembrane domain:**

Amino acids 453-473

**N-glycosylation sites:**Amino acids 118-122;186-190;198-202;211-215;238-242;  
248-252;334-338;357-360;391-395;**Glycosaminoglycan attachment site:**

Amino acids 583-587

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 552-556

**N-myristoylation sites:**Amino acids 107-113;152-158;319-325;438-444;516-522;612-618;  
692-698;696-702;700-706

604/615

**FIGURE 599**

GGTCCTTAATGGCAGCAGCCGCCGCTACCAAGATCCTTCTGTGCCTCCCGCTTCTGCTCCTGC  
TGTCGGGCTGGTCCCGGGCTGGGCGAGCCGACCCTCACTCTCTTTGCTATGACATCACCGTCA  
TCCCTAAGTTTCAGACCTGGACCACGGTGGTGTGCGGTTCAAGGCCAGGTGGATGAAAAGACTT  
TTCTTCACTATGACTGTGGCAACAAGACAGTCACACCTGTCAGTCCCCTGGGGAAGAACTAA  
ATGTCAACAACGGCCTGGAAAGCACAGAACCAGTACTGAGAGAGGTGGTGGACATACTTACAG  
AGCAACTGCGTGACATTCAGCTGGAGAATTACACACCCAAGGAACCCCTCACCTGCAGGCAA  
GGATGTCTTGTGAGCAGAAAGCTGAAGGACACAGCAGTGGATCTTGGCAGTTCAGTTTCGATG  
GGCAGATCTTCCTCCTCTTTGACTCAGAGAAGAGAATGTGGACAACGGTTCATCCTGGAGCCA  
GAAAGATGAAAGAAAAGTGGGAGAATGACAAGGTTGTGGCCATGTCCTTCCATTACTTCTCAA  
TGGGAGACTGTATAGGATGGCTTGAGGACTTCTTGATGGGCATGGACAGCACCCCTGGAGCCAA  
GTGCAGGAGCACCACTCGCCATGTCCTCAGGCACAACCCAACCTCAGGGCCACAGCCACCACCC  
TCATCCTTTGCTGCCTCCTCATCATCCTCCCCTGCTTCATCCTCCCTGGCATCTGAAGGAGAGT  
CCTTTAGAGTGACAGGTTAAAGCTGATACCAAAGGCTCCTGTGAGCACGGTCTTGATCAAAC  
TCGCCCTTCTGTCTGGCCAGCTGCCCACGACCTACGGTGTATGTCCAGTGGCCTCCAGCAGAT  
CATGATGACATCATGGACCCAATAGCTCATTCACTGCCTTGATTCCCTTTTGCCAACAATTTTA  
CCAGCAGTTATACCTAACATATTATGCAATTTTCTCTTGGTGCTACCTGATGGAATTCCTGCA  
CTTAAAGTTCTGGCTGACTAAACAAGATATATCATTTTCTTTCTTCTTTTTGTTTGGAAAA  
TCAAGTACTTCTTTGAATGATGATCTCTTTCTTGCAAATGATATTGTCAGTAAAATAATCACG  
TTAGACTTCAGACCTCTGGGGATTCTTTCCGTGTCTGAAAGAGAATTTTTAAATTATTTAAT  
AAGAAAAAATTTATATTAATGATTGTTTCCTTTAGTAATTTATTGTTCTGTACTGATATTTAA  
ATAAGAGTTCTATTTCCCAAAAAAAAAAAAAAAAAAAAA

605/615

**FIGURE 600**

MAAAAATKILLCLPLLLLLSGWSRAGRADPHSLCYDITVIPKFRPGPRWCAVQGQVDEKTF  
YDCGNKTVTPVSPLGKKLNVTTAWKAQNPVLREVVDILTEQLRDIQLENYTPKEPLTLQARMS  
CEQKAEGHSSGSWQFSFDGQIFLLFDSEKRMWTTVHPGARKMKEKWENDKVVAMSFHYFSMGD  
CIGWLEDFLMGMDSTLEPSAGAPLAMSSGTTQLRATATTLILCCLLIILPCFILPGI

**Important features:**

**Signal peptide:**

amino acids 1-25

**Transmembrane domain:**

amino acids 224-246

**N-glycosylation site.**

amino acids 68-72, 82-86

**N-myristoylation site.**

amino acids 200-206, 210-216

**Amidation site.**

amino acids 77-81

606/615

**FIGURE 601**

GCAGTCAGAGACTTCCCCTGCCCCTCGCTGGGAAAGAACATTAGGAATGCCTTTTAGTGCCTT  
GCTTCCTGAACTAGCTCACAGTAGCCCGGCGGCCAGGGCAATCCGACCACATTTCACTCTCA  
CCGCTGTAGGAATCCAGATGAGGCCAAGTACAGCAGCACGAGGGACATGCTGGATGATGATG  
GGGACACCACCATGAGCCTGCATTCTCAAGCCTCTGCCACAACCTCGGCATCCAGAGCCCCGGC  
GCACAGAGCACAGGGCTCCCTCTTCAACGTGGCGACCAAGTGGCCCTGACCCTGCTGACTTTGT  
GCTTGGTGCTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTCTTTTTCAGTACTACCAGCTCT  
CCAATACTGGTCAAGACACCATTCTCTCAAATGGAAGAAAGATTAGGAAATACGTCCCAAGAGT  
TGCAATCTCTTCAAGTCCAGAATATAAAGCTTGCAGGAAGTCTGCAGCATGTGGCTGAAAAAC  
TCTGTCTGTGAGCTGTATAACAAAGCTGGAGCACACAGGTGCAGCCCTTGTACAGAACAATGGA  
AATGGCATGGAGACAATTGCTACCAGTTCTATAAAGACAGCAAAAGTTGGGAGGACTGTAAAT  
ATTTCTGCCTTAGTGAAAACTCTACCATGCTGAAGATAAACAAGACCTGGAATTTG  
CCGCGTCTCAGAGCTACTCTGAGTTTTTCTACTCTTATTGGACAGGGCTTTTGGCCCTGACA  
GTGGCAAGGCCCTGGCTGTGGATGGATGGAACCCCTTTCACCTCTGAACTGTTCCATATTATAA  
TAGATGTCAACAGCCCCAAGAAGCAGAGACTGTGTGGCCATCCTCAATGGGATCTTCTCAA  
AGGACTGCAAAGAATTGAAGCGTTGTGTCTGTGAGAGAAGGGCAGGAATGGTGAAGCCAGAGA  
GCCTCCATGTCCCCCTGAAACATTAGGCGAAGGTGACTGATTTCGCCCTCTGCAACTACAAAT  
AGCAGAGTGAGCCAGGCGGTGCCAAAGCAAGGGCTAGTTGAGACATTGGGAAATGGAACATAA  
TCAGGAAAGACTATCTCTCTGACTAGTACAAAATGGGTCTCGTGTTTCCTGTTTCAGGATCAC  
CAGCATTCTGAGCTTGGGTTTATGCACGTATTTAACAGTCACAAGAAGTCTTATTTACATGC  
CACCAACCAACCTCAGAAACCCATAATGTCATCTGCCTTCTTGGCTTAGAGATAACTTTTAGC  
TCTCTTTCTTCTCAATGTCTAATATCACCTCCCTGTTTTTCATGTCTTCCTTACACTTGGTGGA  
ATAAGAACTTTTTGAAGTAGAGGAAATACATTGAGGTAACATCCTTTTCTCTGACAGTCAAG  
TAGTCCATCAGAAATTGGCAGTCACTTCCCAGATTGTACCAGCAAATACACAAGGAATTCTTT  
TTGTTTGTTCAGTTCATACTAGTCCCTTCCCAATCCATCAGTAAAGACCCCATCTGCCTTGT  
CCATGCCGTTTCCCAACAGGGATGTCACTTGATATGAGAATCTCAAATCTCAATGCCTTATAA  
GCATTCTTCTGTGTCCATTAAGACTCTGATAATTGTCTCCCTCCATAGGAATTTCTCCCA  
GGAAAGAAATATATCCCCATCTCCGTTTCATATCAGAACTACCGTCCCCGATATTCCCTTCAG  
AGAGATTAAAGACCAGAAAAAAGTGAGCCTCTTCATCTGCACCTGTAATAGTTTCAGTTCCTA  
TTTTCTTCCATTGACCCATATTTATACCTTTCAGGTACTGAAGATTTAATAATAATAAATGTA  
AATACTGTGAAAAA

607/615

**FIGURE 602**

MQAKYSSTRDMLDDDGDTTMSLHSQASATTRHPEPRRTEHRAPSSTWRPVALTLLTLCIVLLI  
GLAALGLLFFQYYQLSNTGQDTISQMEERLGNTSQELQSLQVQNIKLAGSLQHVAEKLCRELY  
NKAGAHRCSPCTEQWKWHGDNCYQFYKDSKSWEDCKYFCLSENSTMLKINKQEDLEFAASQSY  
SEFFYSYWTGLLRPDSGKAWLWMDGTPFTSELFHIIIDVTSPPSRDCVAILNGMIFSKDCKEL  
KRCVCERRAGMVKPESLHVPPETLGEGD

608/615

**FIGURE 603**

GGGAGAGAGGATAAATAGCAGCGTGGCTTCCCTGGCTCCTCTCTGCATCCTTCCCGACCTTCC  
CAGCAATATGCATCTTGACGCTCTGGTCGGCTCCTGCTCCCTCCTTCTGCTACTGGGGGCCCT  
GTCTGGATGGGCGGCCAGCGATGACCCCATTGAGAAGGTCATTGAAGGGATCAACCGAGGGCT  
GAGCAATGCAGAGAGAGAGAGGTGGGCAAGGCCCTGGATGGCATCAACAGTGGAATCACGCATGC  
CGGAAGGGAAGTGGAGAAGGTTTTCAACGGACTTAGCAACATGGGGAGCCACACCGGCAAGGA  
GTTGGACAAAGGCGTCCAGGGGCTCAACCACGGCATGGACAAGGTTGCCCATGAGATCAACCA  
TGGTATTGGACAAGCAGGAAAGGAAGCAGAGAAGCTTGGCCATGGGGTCAACAACGCTGCTGG  
ACAGGCCGGGAAGGAAGCAGACAAAGCGGTCCAAGGGTTCCACACTGGGGTCCACCAGGCTGG  
GAAGGAAGCAGAGAACTTGGCCAAGGGGTCAACCATGCTGCTGACCAGGCTGGAAAGGAAGT  
GGAGAAGCTTGGCCAAGGTGCCACCATGCTGCTGGCCAGGCCGGGAAGGAGCTGCAGAATGC  
TCATAATGGGGTCAACCAAGCCAGCAAGGAGGCCAACAGCTGCTGAATGGCAACCATCAAAG  
CGGATCTTCCAGCCATCAAGGAGGGGCCACAACCACGCCGTTAGCCTCTGGGGCCTCAGTCAA  
CACGCCTTTCATCAACCTTCCCGCCCTGTGGAGGAGCGTCGCCAACATCATGCCCTTAAACTGG  
CATCCGGCCTTGCTGGGAGAATAATGTCGCCGTTGTCACATCAGCTGACATGACCTGGAGGGG  
TTGGGGGTGGGGGACAGGTTTCTGAAATCCCTGAAGGGGTTGTACTGGGATTTGTGAATAAA  
CTTGATACACCA

609/615

**FIGURE 604**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66675
><subunit 1 of 1, 247 aa, 1 stop
><MW: 25335, pI: 7.00, NX(S/T): 0
MHLARLVGSCSLLLLLGALSGWAASDDPIEKVIEGINRGLSNAEREVGKALDGINSGITHAGR
EVEKVFNGLSNMGSHTGKELDKGVQGLNHGMDKVAHEINHGIGQAGKEAEKLGHGVNNAAGQA
GKEADKAVQGFHTGVHQAGKEAEKLGQGVNHAADQAGKEVEKLGQGAHHAAGQAGKELQNAHN
GVNQASKEANQLLNGNHQSGSSSHQGGATTTPLASGASVNTPFINLPALWRSVANIMP
```

**Important features of the protein:****Signal peptide:**

amino acids 1-25

**Homologous region to circumsporozoite (CS) repeats:**

amino acids 35-225



610/615

**FIGURE 605**

GCGACGCGCGGCGGGGCGGCGAGAGGAAACGCGGCGCCGGGCGGGCCCGGCCCTGGAGATGG  
TCCCCGGCGCCGCGGGCTGGTGTGTCTCGTGCTCTGGCTCCCCGCGTGCGTCGCGGGCCACG  
GCTTCCGTATCCATGATTATTTGTACTTTCAAGTGCTGAGTCCTGGGGACATTCGATACATCT  
TCACAGCCACACCTGCCAAGGACTTTGGTGGTATCTTTCACACAAGGTATGAGCAGATTCACC  
TTGTCCCCGCTGAACCTCCAGAGGCCTGCGGGGAACTCAGCAACGGTTTCTTCATCCAGGACC  
AGATTGCTCTGGTGGAGAGGGGGGCTGCTCCTTCCTCTCCAAGACTCGGGTGGTCCAGGAGC  
ACGGCGGGCGGGCGGTGATCATCTCTGACAACGCAGTTGACAATGACAGCTTCTACGTGGAGA  
TGATCCAGGACAGTACCCAGCGCACAGCTGACATCCCCGCCCTCTTCCTGCTCGGCCGAGACG  
GCTACATGATCCGCCGCTCTCTGGAACAGCATGGGCTGCCATGGGCCATCATTTCATCCCAG  
TCAATGTCACCAGCATCCCCACCTTTGAGCTGCTGCAACCGCCCTGGACCTTCTGGTAGAAGA  
GTTTGTCCACATTCCAGCCATAAGTGACTCTGAGCTGGGAAGGGGAAACCCAGGAATTTTGC  
TACTTGGAATTTGGAGATAGCATCTGGGGACAAGTGAGCCAGGTAGAGGAAAAGGGTTTGGG  
CGTTGCTAGGCTGAAAGGGAAGCCACCACTGGCCTTCCCTTCCCAGGGCCCCCAAGGGTG  
TCTCATGCTACAAGAAGAGGCAAGAGACAGGCCCCAGGGCTTCTGGCTAGAACCCGAAACAAA  
AGGAGCTGAAGGCAGGTGGCCTGAGAGCCATCTGTGACCTGTCACACTCACCTGGCTCCAGCC  
TCCCCTACCCAGGGTCTCTGCACAGTGACCTTCACAGCAGTTGTTGGAGTGGTTAAAGAGCT  
GGTGTGTTGGGACTCAATAAACCTCACTGACTTTTTAGCAATAAAGCTTCTCATCAGGGTTG  
CAAAAAAAAAAAAAAAAAAAAAAAAAA

611/615

**FIGURE 606**

&gt;&lt;/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76532

&gt;&lt;subunit 1 of 1, 188 aa, 1 stop

&gt;&lt;MW: 21042, pI: 5.36, NX(S/T): 2

MVPGAAGWCCLVLWLPACVAAHGFRIHDYLYFQVLSPGDIRYIFTATPAKDFGGIFHTRYEQI

HLVPAEPPEACGELSNGFFIQDQIALVERGGCSFLSKTRVVQEHGGRAVIISDनावDNDsfyv

EMIQDSTQRTADIPALFLLGRDGYMIRRSLEQHGLPWAIISIPVNVTSIPTFELLQPPWTFW

**Signal peptide:**

amino acids 1-20

612/615

**FIGURE 607**

GCATTTGCCACTGGTTGCAGATCAGGCGGACGAGGAGCCGGGAAGGCAGAGCC**ATG**TGGCTGC  
CCCCTGCTCTGCTCCTTCTCAGCCTCTCAGGCTGTTTCTCCATCCAAGGCCAGAGTCTGTGA  
GAGCCCCAGAGCAGGGGTCCCTGACGGTTCAATGCCACTATAAGCAAGGATGGGAGACCTACA  
TTAAGTGGTGGTGGCGAGGGGTGCGCTGGGATACATGCAAGATCCTCATTGAAACCAGAGGGT  
CGGAGCAAGGAGAGAAGAGTGACCGTGTGTCCATCAAGGACAATCAGAAAGACCGCACGTTCA  
CTGTGACCATGGAGGGGCTCAGGCGAGATGACGCAGATGTTTACTGGTGTGGGATTGAAAGAA  
GAGGACCTGACCTTGGGACTCAAGTGAAAGTGATCGTTGACCCAGAGGGAGCGGCTTCCACAA  
CAGCAAGCTCACCTACCAACAGCAATATGGCAGTGTTTCATCGGCTCCCACAAGAGGAACCACT  
ACATGCTCCTGGTATTTGTGAAGGTGCCCATCTTGCTCATCTTGGTCACTGCCATCCTCTGGT  
TGAAGGGGTCTCAGAGGGTCCCTGAGGAGCCAGGGGAACAGCCTATCTACATGAACCTCTCCG  
AACCTCTGACTAAAGACATGGCCACT**TAG**AGAGATGGATCTGCAGAGCCTTCTGCCCTGGCC  
ACGTTTCCAGAAGAGACTCGGGCTGTGGAAGGAACATCTACGAGTCCTCGGGATGCAGTGACT  
GAGATAGGGGCCCTGGGCCTCCGCCCTGGCCTTGAGAGCTGGTGGGCACCTCCCTGTTCTGCAC  
AGCTCAGGGACTTAGCCAGGTCTCTCTGAGCCACCATCACCTCCTGGGGTGCCAGCACCTG  
TTCTCTTGGTCAGGAGCTGTAGAGATGGAGCTCAAGCACTGGACGACTCTGTCCCCACTGCTG  
GAATAACTCGGGCACAGAGCATGGGACCAAAGTACAGAAAGAGGTGGGGGAGACCCCCCAG  
CCCTAGACTTCCATCATTCCGGAGACCAACTCAACACCGTCTTTGCCTGAGAACCTGATATATCC  
GTGTTTTTAAATTTTTTTTTTCTAGCAAAGTTGGGTTTTAATGACTTATGTTTCATAGGAAAC  
CTCTCTGATCCACACACAAGGAGGGTGATTCTGGGATGAGTTCCTGGTTCTAGGGCATGAGG  
GGCTGGATGGACCTGTCCCCAGGGAGGACATGGCTCTGAGTCCACAGGGCTGAGGAGGCAAT  
GGGAACCTCCCTGGCCCGGCCCGGTGCTTGTCTCCCCCTCCCACCTCTTCTCTCTCTAGCT  
CCCCAAGCTCCCTGCCTATTCCCCCACCTCCGAGGGGCTGCAGCTTGGGAGCCTCCTCAGCAT  
GACAGCTTGGGTCTCTCCCCAAAAGAGCCTGTCAGGCCTCAAGAACCACCTCCAGGTGGGGA  
GGGCAGTAACGAAAACCATCGCAGGAAATGGCACCCCTCCCTTTTCGGTGATGTTGAAATCATG  
TTACTAATGAAAACGTCTCTAGGGAAGTGGTTCTGTCTCCTCACAGGCTTCACCCACGGCGAT  
GAGGCCCTTGAATGTGGTCACTTTGTGCTGTATGGTTGAGGGACCCTCACACCAAAGGGACCT  
TCCCATGTGAGATGTGCTCCCGCCCCCACCTGCCACAAAGCAAACACACCACACATGTTCCGC  
ATGTTGCCCTTTGAACACCCATGAGGACGCCTCCAACCTGCTCTTGGTTCTAATAGGGAGTAC  
TGACTGTCAGCAGTGGATAAAGGAGAGGGGACCCTCTGGTCCCTAGCATGGCACCCAGAGCCT  
CCCCTCTTCTTGTCTTCTCAGCCAAAGAGAACTTTCTCTGACTTTGAACTGAATTTAGGTCTC  
TGGCCAATGATGGGCCTGAAAATTCATAATGGCCAGAGAGGAGAGTTCGAGCCCGGCTAAGA  
TCCCCTGAGTCATTCTGTGAGGGACCAAGACCCACAGTCCACCAGCCCCAGGGCCCTACCTCC  
TGGAATGCTTTCTTGGATCCAGCTTCCCGAAGATCCGACCAGACCCAGGGAGGACGGCACCGC  
TCCGCGGGAGGGAAAGCCAAAGCATGGTGCTTACCAGCTGGACTCAGGGGCGAGGGGACATG  
GGCGCTTGTCAACGTGATGTCATTCTTTTCCACCGTTTCTTCTGTTGATATTCAATGAATC  
CGTCAATCTCTCTGGGAAA

613/615

**FIGURE 608**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA105849
><subunit 1 of 1, 201 aa, 1 stop
><MW: 22689, pI: 7.41, NX(S/T): 1
MWLPPALLLLSLSGCFSIQGPESVRAPEQGSLTVQCHYKQGWETYIKWWCRGVRWDTCIKI
LIETRGEQGEKSDRVSIKDNQKDRTFTVTMEGLRRDDADVWCGIERRGPDLTQVKVI
VDPEGAASTTASSPTNSNMAVFIGSHKRNHMYLLVFVKVPILLILVTAILWLKGSQRPVE
EPGEQPIYMNFFSEPLTKDMAT
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-17

**Transmembrane domain:**

Amino acids 151-170

**N-glycosylation site:**

Amino acids 190-194

**Tyrosine kinase phosphorylation site:**

Amino acids 95-103

**N-myristoylation sites:**

Amino acids 66-72;125-131

**Prokaryotic membrane lipoprotein lipid attachment site:**

Amino acids 5-16

614/615

**FIGURE 609**

GATGGCGCAGCCACAGCTTCTGTGAGATTTCGATTTCTCCCCAGTTCCCCTGTGGGTCTGAGGG  
GACCAGAAGGGTGAGCTACGTTGGCTTTCTGGAAGGGGAGGCTATATGCGTCAATTCCCCAAA  
ACAAGTTTTGACATTTCCCCTGAAATGTCATTCTCTATCTATTCACTGCAAGTGCCTGCTGTT  
CCAGGCCTTACCTGCTGGGCACTAACGGCGGAGCCAGGATGGGGACAGAATAAAGGAGCCACG  
ACCTGTGCCACCAACTCGCACTCAGACTCTGAACTCAGACCTGAAATCTTCTCTTCACGGGAG  
GCTTGGCAGTTTTTCTTACTCCTGTGGTCTCCAGATTTCAGGCCTAAGATGAAAGCCTCTAGT  
CTTGCCTTCAGCCTTCTCTGCTGCGTTTTATCTCCTATGGACTCCTTCCACTGGACTGAAG  
ACACTCAATTTGGGAAGCTGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTCT  
GAGATACGGGGCAGTGTGCAAGCCAAAGATGGAACATTGACATCAGAATCTTAAGGAGGACT  
GAGTCTTTGCAAGACACAAAGCCTGCGAATCGATGCTGCCTCCTGCGCCATTTGCTAAGACTC  
TATCTGGACAGGGTATTTAAAAACTACCAGACCCCTGACCATTATACTCTCCGGAAGATCAGC  
AGCCTCGCCAATTCCTTTCTTACCATCAAGAAGGACCTCCGGCTCTCTCATGCCCCACATGACA  
TGCCATTGTGGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTG  
GAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAAGTAGACATTCTTCTGCAATGGATGGAG  
GAGACAGAAATAGGAGGAAAGTGATGCTGCTGCTAAGAATATTCGAGGTCAAGAGCTCCAGTCT  
TCAATACCTGCAGAGGAGGCATGACCCCAAACCATCTCTTTACTGTACTAGTCTTGTGCT  
GGTCACAGTGTATCTTATTTATGCATTACTTGCTTCCTTGCATGATTGTCTTTATGCATCCCC  
AATCTTAATTGAGACCATACTTGTATAAGATTTTTGTAATATCTTTCTGCTATTGGATATATT  
TATTAGTTAATATATTTATTTATTTTTTGGCTATTTAATGTATTTATTTTTTTACTTGGACATG  
AACTTTAAAAAAATTCACAGATTATATTTATAACCTGACTAGAGCAGGTGATGTATTTTTAT  
ACAGTAAAAAATAAACCTTGTAATTCTAGAAGAGTGGCTAGGGGGGTTATTCATTTGTAT  
TCAACTAAGGACATATTTACTCATGCTGATGCTCTGTGAGATATTTGAAATTGAACCAATGAC  
TACTTAGGATGGGTTGTGGAATAAGTTTTGATGTGGAATTGCACATCTACCTTACAATTACTG  
ACCATCCCCAGTAGACTCCCCAGTCCCATAATTGTGTATCTTCCAGCCAGGAATCCTACACGG  
CCAGCATGTATTTCTACAAATAAAGTTTTCTTTGCATACCAAAAAAAAAAAAAAAAAAAAAA

615/615

**FIGURE 610**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA83500
><subunit 1 of 1, 261 aa, 1 stop
><MW: 29667, pI: 8.76, NX(S/T): 0
MRQFPKTSFDISPEMSFSIYSLQVPAVPG LTCWALTAEPGWGQNKGATTCATNSHSDSEL
RPEIFSSREAWQFFLLWSPDFRPKMKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVI
ATNLQEIRNGFSEIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVF
KNYQTPDHYTLRKISSLANSTLTIKKDLRLSHAMTCHCGEAMKKYSQILSHFEKLEPQ
AAVVKALGELDILLQWMEETE
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-42

**cAMP- and cGMP-dependent protein kinase phosphorylation sites:**

Amino acids 192-196;225-229

**N-myristoylation sites:**

Amino acids 42-48;46-52;136-142

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20 December 2000 (20.12.2000) US
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- (72) Inventors; and
- (75) Inventors/Applicants (for US only): BAKER, Kevin, P. [GB/US]; 14006 Indian Run Drive, Darnestown, MD 20878 (US). CHEN, Jian [US/US]; 121 York Drive, Princeton, NJ 08540 (US). DESNOYERS, Luc [CA/US]; 2050 Stockton Street, San Francisco, CA 94133 (US). GODDARD, Audrey [CA/US]; 110 Congo Street, San Francisco, CA 94131 (US). GODOWSKI, Paul, J. [US/US]; 2627 Easton Drive, Burlingame, CA 94010 (US). GURNEY, Austin, L. [US/US]; 1 Debbie Lane, Belmont, CA 94002 (US). PAN, James [CA/US]; 2705 Coronet Boulevard, Belmont, CA 94002 (US). SMITH, Victoria [AU/US]; 19 Dwight Road, Burlingame, CA 94010 (US). WATANABE, Colin, K. [US/US]; 128 Corliss Drive, Moraga, CA 94556 (US). WOOD, William, I. [US/US]; 35 Southdown Court, Hillsborough, CA 94010 (US). ZHANG, Zemin [CN/US]; 876 Taurus Drive, Foster City, CA 94404 (US).
- (74) Agents: BARNES, Elizabeth, M. et al.; c/o Genentech, Inc., MS49, 1 DNA Way, South San Francisco, CA 94080-4990 (US).
- (81) Designated States (national): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.
- (84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

[Continued on next page]

(54) Title: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME

(57) Abstract: The present invention is directed to novel polypeptides and to nucleic acid molecules encoding those polypeptides. Also provided herein are vectors and host cells comprising those nucleic acid sequences, chimeric polypeptide molecules comprising the polypeptides of the present invention fused to heterologous polypeptide sequences, antibodies which bind to the polypeptides of the present invention and to methods for producing the polypeptides of the present invention.

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*For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.*

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## INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 01/06520

## A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12N15/12 C12N15/62 C07K14/47 C07K14/705 C07K16/18  
G01N33/53 C12Q1/68

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

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Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, WPI Data, PAJ, BIOSIS, SEQUENCE SEARCH

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

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☒ Further documents are listed in the continuation of box C.☒ Patent family members are listed in annex.

## \* Special categories of cited documents :

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"P" document published prior to the international filing date but later than the priority date claimed

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"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"Z" document member of the same patent family

Date of the actual completion of the international search

28 February 2002

Date of mailing of the international search report

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Name and mailing address of the ISA

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Oderwald, H

## INTERNATIONAL SEARCH REPORT

Internatic..... Application No

PCT/US 01/06520

## C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

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# INTERNATIONAL SEARCH REPORT

International application No.  
PCT/US 01/06520

## Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.:  
because they relate to subject matter not required to be searched by this Authority, namely:  
  
Although claims 20 and 21 are directed to a method of treatment of the human/animal body (in so far as in vivo methods are concerned), the search has been carried out and based on the alleged effects of the compound/composition.
2. ☐ Claims Nos.:  
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:  
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

## Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:  
  
1-24 (all partially)

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

Invention 1: claims 1-24 partially

^ An isolated nucleic acid SEQ ID NO: 1 which encodes amino acid sequence SEQ ID NO: 2. A vector, a host cell, a process for producing a polypeptide, an isolated polypeptide encoded by said nucleic acid. A chimeric molecule, an antibody, methods for stimulating the release of TNF-alpha, for stimulating the proliferation or differentiation, for detecting the presence of tumor, an oligonucleotide probe.

Inventions 2-305: claims 1-24 partially

same as invention 1 but comprising the polynucleotide and amino acid sequence in the order given in claims 1 and 2 (invention 2 is limited to SEQ ID NO: 3 and 4 and invention 305 is limited to SEQ ID NO: 609 and 610).

## INTERNATIONAL SEARCH REPORT

Information on patent family members

Internatic..... Application No

PCT/US 01/06520

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Information on patent family members

International Application No

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